





XX	AAV57594:
AC	
DT	02-MAR-2000 (first entry)
DE	Human Wnt-1 protein.
XX	
KW	Wnt-1; neuronal growth; differentiation; regeneration;
KM	dorsal neural progenitor cell; neurodegenerative disease;
KM	Parkinson's disease; amyotrophic lateral sclerosis;
KM	diffuse Lewy body disease; cortical-basal ganglionic degeneration;
KW	Hallervorden-Spatz disease; myoclonic epilepsy.
XX	
OS	Homo sapiens.
XX	
FN	M09957248-A1.
PD	
XX	11-NOV-1999.
FE	
XX	30-APR-1998: 98WD-US08715.
PR	
XX	30-APR-1998: 98WD-US08715.
PA	(HARD) HARVARD COLLEGE.
XX	
E1	McMahon AP, Lee SK, Takada S;
DR	WPI: 2000-062145/05.
DP	N-PSTB: AAZ17789.
PT	Fetched populations of mammalian neural precursor cells for treating Parkinson's disease .
PS	Claim 6; Page 4; 57pp; English.
XX	
CC	The present invention describes an enriched population of mammalian neural precursor cells committed to a cell fate, the cells being characterized in that they exhibit a stem cell phenotype in the presence of a Wnt polypeptide but not in the absence of the Wnt polypeptide.
CC	The enriched population of dopaminergic neuron precursor cells can be used in a method for treating Parkinson's disease. The enriched population of dorsal neural precursor cells can be used to induce neuronal regenerative disorder in an adult mammal suffering from a neurodegenerative disorder. The disorder that can be treated is Parkinson's disease, Amyotrophic lateral sclerosis, diffuse Lewy body disease, cortical-basal ganglionic degeneration, Hallervorden-Spatz disease or myoclonic epilepsy. The present sequence represents the human Wnt-1 protein.
CC	
XX	
SQ	Sequence 370 AA:
Query Match	100.0%; Score 2036; DR 21; Length 370;
Best Local Similarity	100.0%; Pred. No. 3,9e-195;
Matches 370:	Conservative 0; Mismatches 0; Indels 0; Gaps
Y	1 MGMLALPEWWSATLLTALAALPALANSSGRMWIVWASTLTLDKSLQVLTPS 60
DB	1 MGMLALPGWSAALLLALCALPALANSSGRMWIYWASTLTLDKSLQLTERS 60
Y	61 LGLLSKRQELFRONPGLTHSVSGGLASVAEREKWFFRRRRKNCTAFAGHLGKIYVRG 120
DB	61 LGLLSKRQELFRILRONPGLTHSVSGGLASVAEREKWFFRRRRKNCTAFAGHLGKIYVRG 120
Y	121 GRETAIFAITSACVTISVASRCSEGSTESCTCDYERRRGSPGMHWGGSDNIDFGKLF 180
DB	121 GRETAIFAITSACVTHSVARSCEGSTIESCTCDYERRRGSPGMHWGGSDNIDFGKLF 180
Y	181 GREPVDSGSKRPDLRFIMNLHNNEAGRTTVSEMGCEKCHMSGSCTVTCMKPLFTLP 240
DB	181 GREPVDSGSKRPDLRFIMNLHNNEAGRTTVSEMRCKCHMSGSCTVTCMKRLPLTR 240
Y	241 AVGDVLRDFDGASRVLYGNRGSNRASAEILLREPEDPARKPSPHDLYVEKSPNCT 300
DB	241 AVGDVLRDFDGASRVLYGNRGSNRASAEILLREPEDPARKPSPHDLYVEKSPNCT 300

[illegible]

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Db      61  LQLLSKKQRLIRONPGILHSVSGLSQAVRECKWQFENRKNWCPDAPGPHLFGKIVNR3 120
QY      121  CRETAIFAITSAGVTHSVARSCESSIESCTCDYRKHGQGGPDHMGCSNDINDEGRLE 180
Db      121  CRETAIFAITSAGVTHSVARSCESSIESCTCDYRKHGQGGPDHMGCSNDINDEGRLE 180
QY      181  GREFYVSGEKQGLDFRLMNLHNEAGRTTVESEMRQCKHGKSSGCTVRCWRLPTLR 240
Db      181  GREFYVSGEKQGLDFRLMNLHNEAGRTTVESEMRQCKHGKSSGCTVRCWRLPTLR 240
QY      241  AVGDVLRDPFGASRVLYGNRGSNRASRAELLRLPEPDPAHKPPSHDLVYFEKSPNCT 300
Db      241  AVGDVLRDPFGASRVLYGNRGSNRASRAELLRLPEPDPAHKPPSHDLVYFEKSPNCT 300
QY      301  YSGRLTAGTAGRACNSSSPALDGCGRGHRITQPTQVTERQCNCFHWCCHVSCRNC 360
Db      301  YSGRLTAGTAGRACNSSSPALDGCGRGHRITQPTQVTERQCNCFHWCCHVSCRNC 360
QY      361  THTRVLECL 370
Db      361  THTRVLECL 370

RESULT 5
ABB61007
ID      ABB61007 standard; Protein; 468 AA.
XX
AC      ABB61007;
XX
DT      26-MAR-2002 (first entry)
XX
DE      Drosophila melanogaster polypeptide SEQ ID NO 9813.
XX
KW      Drosophila; developmental biology; cell signalling; insecticide;
KW      pharmaceutical.
XX
SS      Drosophila melanogaster.
XX
PN      WO200171042-A2.
XX
PD      27-SEP-2001.
XX
PF      23-MAR-2001; 2001WO-US09231.
XX
PR      23-MAR-2000; 2000US-191637P.
XX
PR      11-JUL-2000; 2000US-0614150.
XX
PA      (PEKE ) PE CORP NY.
XX
V       Venter JC, Adams M, Li PMD, Myers EW:
        WPI: 2001-656860/75.
        N-PSDB: AB105110.
XX
PT      New isolated nucleic acid detection reagent for detecting 1000 or more
        genes from Drosophila and for elucidating cell signalling and cell-cell
        interactions.
XX
PS      Disclosure: SEQ ID NO 9813; 21pp + Sequence Listing; English.
XX
CC      The invention relates to an isolated nucleic acid detection reagent
        capable of detecting 1000 or more genes from Drosophila. The invention is
        useful in developmental biology and in elucidating cell signalling and
        cell-cell interactions in higher eukaryotes for the development of
        insecticides, therapeutics and pharmaceutical drugs. The invention
        discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
        sequences (AB101840-AB116175) and the encoded proteins
        (AB85737-AB872072).
CC      The sequence data for this patent did not form part of the printed
        specification, but was obtained in electronic format directly from WIPO
        at ftp.wipo.int/pub/published_pct_sequences.
XX

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SQ      Sequence      468 AA:
Query Match      50.2%; Score 1022.5; Db 42; Length 468;
Best Local Similarity 45.7%; Pred. No. 1,66-93;
Matches 203; Conservative 43; Mismatches 89; Indels 109; Gaps 6;

QY      31  SGR-----WGIIVVASSTNLLTDSKSLQVLEPSL-QLLSKQGRFLIRONPGILHSVSG 84
Db      30  SGRGSGSMWGIIVASVGEPNNI-----TPIYMDPAIHSTLRKQARLEKONPGVIGALVX 84
QY      85  GLQSAVRECKWQFENRKNWCPD---APGPHLFGKIVNRGCRETAIFAITSAGVTHSVAR 141
Db      85  GANLAISSCQHQFENRKNWCPDSTRNSRGNLFGKIVDRGCRETSPIVAITSAGVTHSIAR 144
QY      142  SCSEGSIESCTCDY--RRGP-----GGPDHMGCSNDINDEGRLEFGREYVDSGE 169
Db      145  ACSSEGIIESCTCDYSHQSRSPQANHQAQSVAGVADWEGWGCSDNIGSFYKFSREYVDGE 204
QY      190  KGRDLRFLMNLHNEAGRTTVESEMRQCKHGKSSGCTVRCWRLPTLRVAVDYLDR 249
Db      205  RGNLRERKNLHNEAGRAHVAQAEKMRQCKHGKSSGCTVRCWRLANFRVIGDLKAR 264
QY      250  PDGASRVLYGN-----RGSNRASRAELL----- 272
Db      265  FDCATRVQVNTSLRATNALAPVSPNAGSNSVSGNGLIPQSGLYVSEEEERLNDHMPD 324
QY      273  -----RLEPDPAHKPPSP 286
Db      325  ILLENSHPISKIHHPNPSNLSLPGQGRGGRNGRQGRKRNHAFPLNHNHEKPPSS 384
QY      287  HDLVYFEKSPNCTYSGRLTAGTAGRACNSSSPALDGCGRGHRITQPTQVTERQCN 346
Db      385  KDLVYLESPSPFCEKKNLQGIILCTHGRQCNETSLGVDSGLMCCGPRVYFDEYVVERCA 444
QY      347  CTFHWCCHVSCRNCTHTRVLECL 370
Db      445  CTFHWCCEVKCKLCRTIKVIYTCL 468

RESULT 6
AAV57596
ID      AAV57596 standard; Protein; 352 AA.
XX
AC      AAV57596;
XX
DT      02-MAR-2000 (first entry)
XX
DE      Murine Wnt-3a protein.
XX
KW      Wnt-1; neuronal growth; differentiation; regeneration;
KW      dorsal neural progenitor cell; neurodegenerative disease;
KW      Parkinson's disease; amyotrophic lateral sclerosis;
KW      diffuse Lewy body disease; cortical-basal ganglionic degeneration;
KW      Hallervorden-Spatz disease; myoclonic epilepsy.
XX
OS      Mus sp.
XX
PN      WO957248-A1.
XX
PD      11-NOV-1999.
XX
PF      30-APR-1998; 98WO-US08716.
XX
PR      30-APR-1998; 98WO-US08716.
XX
PA      (HARD ) HARVARD COLLEGE.
XX
PI      McMahon AP, Lee SK, Takada S;
XX
DR      WPI: 2000-062145/05.
XX
DR      N-PSDB: AA247790.
XX
PT      Enriched populations of mammalian neural precursor cells, for treating

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QY 134 GYHSAVSCSESSIESCTCDYKRRGPGSPMHM337SDNIDFGRLPERFVDSGEKR- 192
DB 119 GAFAVTRACSGDELEKCGDRTVGVSPGFWSGSNDINAVGAVSQSVDVREKSG 178
QY 193 --DLFELNNLNNEAGRTVFSEMRQCKGSGSCTVCTOMKPLPLRAVDVLDPE 250
DB 179 ASSSRALNNLNNEAGRKALITMRVECKCHGVSGCEVKCTOMRAVPEPQVGHAKKE 238
QY 251 DGSARVLGNNGSGNRASRAELRLEREDPAKRPSPHDLVFEKSPNFCITSGRLTACT 310
DB 239 DGAIVFPRVGSRA-----LVPRNAOKRPHLEDELVLESPDFCEQDMRSGVGI 291
QY 311 AFRANSSPALDGCCLDGGCRHRTQRYTEMNCTIMWQVHVSCKNTIHTVACHQ 369
DB 292 RGRCTNKTKSKALDGCCLDGGCRHRTQRYTEMNCTIMWQVHVSCKNTIHTVACHQ 291

RESULT 9
AAB44275
ID AAB44275 standard: Protein: 351 AA.
XX
XX AAB44275:
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PR0964 (UW426) protein sequence SEQ ID NO:226.
XX
KW Human: secreted protein; transmembrane protein; PRO; EST; cytosolic;
KM expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN W0200053756-A2.
PD 14-SEP-2000.
XX
XX 18-FEB-2000: 2000MO-US04141.
XX
PR 08-MAR-1999: 99MO-US05028.
PR 12-MAR-1999: 99OS-023457.
PR 29-MAR-1999: 99OS-0126773.
PR 21-APR-1999: 99OS-0130232.
PR 28-APR-1999: 99OS-0131445.
PR 14-MAY-1999: 99OS-0134287.
PR 23-JUN-1999: 99OS-0141037.
PR 26-JUL-1999: 99OS-0145698.
PR 29-OCT-1999: 99OS-0162506.
PR 30-NOV-1999: 99OS-0162813.
PR 02-DEC-1999: 99MO-US28551.
PR 16-DEC-1999: 99MO-US28565.
PR 30-DEC-1999: 99MO-US31095.
PR 30-DEC-1999: 99MO-US31243.
PR 05-JAN-2000: 2000MO-US00219.
PR 06-JAN-2000: 2000MO-US00272.
PR 06-JAN-2000: 2000MO-US00376.
XX
XX (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Busuyets L, Eaton DL,
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerltsen NE,
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoi NF, Roy MA,
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI.
DR WPI: 2000-611443/58.
DR N-PSDB: AAC78505.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods,
PI to target bioactive molecules to specific cells, and to modulate
PI cellular activities -
XX
XX Claim 12: Fig 83: 636pp: English.

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XX AAC78458 to AAC7859: represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells.
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78980 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.
XX
SQ Sequence: 351 AA:
Query Match 41 3% Score 849.00 DP 210 Length 351
First Local Similarity 44 3% Prod. No. 210-75
Matches 161 Conservative 553 Mismatches 122 Gaps 20 Gaps 4:

QY 14 TLTAALALPALAANSSGKMMQIVNASSINILNLSKLVAVHSTALSKQRLIR 73
DB 9 SRLVAVFVSSAASN-----MLVLAKLVSQSISEETICE-----KLKMLQVQMK 58
QY 14 QNESTLGVSSLLGSAVRDQWQVNRKRNPTAPGHLEQVYVPELAFVATISA 133
DB 59 RNLEMDVVRKQALATERVLFENRHNSTLDELPAVQVVTTHRAAVVAISSA 218
QY 134 GYHSAVSCSESSIESCTCDYKRRGPGSPMHM337SDNIDFGRLPERFVDSGEKR- 192
DB 119 GAFAVTRACSGDELEKCGDRTVGVSPGFWSGSNDINAVGAVSQSVDVREKSG 178
QY 193 --DLFELNNLNNEAGRTVFSEMRQCKGSGSCTVCTOMKPLPLRAVDVLDPE 250
DB 179 ASSSRALNNLNNEAGRKALITMRVECKCHGVSGCEVKCTOMRAVPEPQVGHAKKE 238
QY 251 DGSARVLGNNGSGNRASRAELRLEREDPAKRPSPHDLVFEKSPNFCITSGRLTACT 310
DB 239 DGAIVFPRVGSRA-----LVPRNAOKRPHLEDELVLESPDFCEQDMRSGVGI 291

RESULT 10
AAV57270
ID AAV57270 standard: Protein: 351 AA.
XX
XX AAV57270:
XX
DT 06-JUN-2000 (first entry)
XX
DE Wnt-4AF and Wnt-5C homolog polypeptide #1.
XX
KW Wnt: Wnt-4AF; Wnt-5C; frizzled gene; membrane protein; diagnostic;
KM therapeutic; human.
XX
OS Homo sapiens.
XX
PN W0200012117-A1.
PD 06-MAR-2000.
XX
XX 31-AUG-1999: 98OS-0092443.
XX 31-AUG-1999: 98OS-0094553.
XX 30-OCT-1999: 98OS-0104452.
XX 01-DEC-1999: 98OS-0115065.
XX
XX (GETH) LITTE & CO LTD.
XX
XX Claim 12: Fig 83: 636pp: English.

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XX
DR WPI: 2000-256491/22.
DR N-PSDB: AA290451.
XX
PT New gene encoding the Wnt-4AF and Wnt-5C homolog polypeptide
PT in developmental control during embryonic development is useful to
PT diagnose and treat related disease
XX
PS Claim 9: Page 72-73; 41pp; English.
XX
CC The invention provides isolated nucleic acid sequences (AA290451-454)
CC encoding Wnt-4AF and Wnt-5C homolog polypeptides (AA29270-273). The
CC polypeptides can be expressed by standard recombinant methodology. They
CC upregulate gene expression by binding to frizzled class of membrane
CC proteins. The Wnt antibodies can be used in diagnostics and therapeutics,
CC while chimeric and transgenic animals can provide models of disease for
CC testing the effectiveness of therapeutic or diagnostic agents.
XX
SQ Sequence 351 AA:
Query Match 41.3%; Score 840; DB 21; Length 351;
Best Local Similarity 44.6%; Pred. No. 2,1e-75;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;
QY 14 TLLALALPALAALANSSGPMWIVNVAASINLLTDSKSLQVLEPFLSLSKQKRLIR 73
DB 9 SLRLVFAVFAASAASN-----WLYLAKLSVGSISSEETEE-----KLKGLIQRYOMCK 58
QY 74 QNPGILHSVSGILQSAVERCKWQFNRKNCPTAPGPHLEKIVNRGPHETAFATISA 133
DB 59 RNLEWDSVFRGAQLAIEECYQYFRRNRKNCSTLSPVFGKVVYQGTREAFVYATISA 118
QY 134 GVHSVARSCESSIECTDYRRKRGPGPMMHMGSGSDNIDFGKLFKRGVDSGKGR 192
DB 119 GVAFATIRAGSGGELKRGSDRIYHVSFGQFWSGSDNIAGVAFVLSVDPVPSKRG 178
QY 193 --DLRFIMLNHNNEAGRTVFSSEMRQCKHMSGSGTVPATCMKRLPLRAVGVLDPRF 250
DB 179 ASSRFALMNLHNNEAGRKALITHMVECKCHGVSCEVATCWRAVPPFGVGHALKERF 238
QY 251 DGASRYLVNRSNASHRAELTLEPEDPAHKPPSPHICLVYFEKSNFTTSCHLSTAGT 310
DB 239 DGATVEHFRVYSSRA-----LVPRNAQKPHIDELVILEPSPDFEODMSVLDGT 291
QY 311 AGACNSSSFALDGLDGGGRHPTFGVTERONCTTHMGCHVSGRNTHTRVLEHG 369
DB 292 RGRCTKRTSKAIDGGLDGGGRHPTAGVLEAERCSKPHMGCFVKTQYFLVELEHTG 350
RESULT 11
Y57273
AA292723 standard: Protein: 351 AA.
AC AA292723;
XX
DT 06-JUN-2000 (first entry)
XX
DE Wnt-4AF and Wnt-5C homolog polypeptide #4.
XX
KM Wnt-4AF; Wnt-5C; frizzled gene; membrane protein; diagnostic;
KM therapeutic; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT MISC-difference 120 /note="encoded by G"
XX
XX W0200012117-A1.
XX
PD 09-MAR-2000.
XX
PF 20-AUG-1999; 99WD-0539045.

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XX
PR 31-AUG-1998; 98US-0096449.
PR 31-AUG-1998; 98US-0096454.
PR 30-OCT-1998; 98US-0106462.
PR 09-DEC-1998; 98US-0111588.
XX
PA (EELI ) LILLY & CO ELLI.
XX
PI Edmunds BI. Su W;
XX
DR WPI: 2000-256491/22.
DR N-PSDB: AA290454.
XX
PT New gene encoding the Wnt-4AF and Wnt-5C homolog polypeptide involved
PT in developmental control during embryonic development is useful to
PT diagnose and treat related disease
XX
PS Claim 9: Page 75-77; 41pp; English.
XX
CC The invention provides isolated nucleic acid sequences (AA290451-474)
CC encoding Wnt-4AF and Wnt-5C homolog polypeptides (AA29270-273). The
CC polypeptides can be expressed by standard recombinant methodology. They
CC upregulate gene expression by binding to frizzled class of membrane
CC proteins. The Wnt antibodies can be used in diagnostics and therapeutics,
CC while chimeric and transgenic animals can provide models of disease for
CC testing the effectiveness of therapeutic or diagnostic agents.
XX
SQ Sequence 351 AA:
Query Match 41.3%; Score 840; DB 21; Length 351;
Best Local Similarity 44.6%; Pred. No. 2,1e-75;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;
QY 14 TLLALALPALAALANSSGPMWIVNVAASINLLTDSKSLQVLEPFLSLSKQKRLIR 73
DB 9 SLRLVFAVFAASAASN-----WLYLAKLSVGSISSEETEE-----KLKGLIQRYOMCK 58
QY 74 QNPGILHSVSGILQSAVERCKWQFNRKNCPTAPGPHLEKIVNRGPHETAFATISA 133
DB 59 RNLEWDSVFRGAQLAIEECYQYFRRNRKNCSTLSPVFGKVVYQGTREAFVYATISA 118
QY 134 GVHSVARSCESSIECTDYRRKRGPGPMMHMGSGSDNIDFGKLFKRGVDSGKGR 192
DB 119 GVAFATIRAGSGGELKRGSDRIYHVSFGQFWSGSDNIAGVAFVLSVDPVPSKRG 178
QY 193 --DLRFIMLNHNNEAGRTVFSSEMRQCKHMSGSGTVPATCMKRLPLRAVGVLDPRF 250
DB 179 ASSRFALMNLHNNEAGRKALITHMVECKCHGVSCEVATCWRAVPPFGVGHALKERF 238
QY 251 DGASRYLVNRSNASHRAELTLEPEDPAHKPPSPHICLVYFEKSNFTTSCHLSTAGT 310
DB 239 DGATVEHFRVYSSRA-----LVPRNAQKPHIDELVILEPSPDFEODMSVLDGT 291
QY 311 AGACNSSSFALDGLDGGGRHPTFGVTERONCTTHMGCHVSGRNTHTRVLEHG 369
DB 292 RGRCTKRTSKAIDGGLDGGGRHPTAGVLEAERCSKPHMGCFVKTQYFLVELEHTG 350
RESULT 12
AA2929063
IT AA2929063 standard: Protein: 351 AA.
AC AA2929063;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human pro polypeptide sequence #40.
XX
KM PRO polypeptide; mammal; tumour; cancer; human; cat; dog; horse; sheep;
KM dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KM blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KM adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX

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OS Homo sapiens.  
 XX  
 PN W0200168848-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 28-FEB-2001: 2001W0-US06520.  
 XX  
 PR 01-MAR-2000: 2000W0-US05601.  
 PR 02-MAR-2000: 2000W0-US05841.  
 PR 03-MAR-2000: 2000US-187202P.  
 PR 06-MAR-2000: 2000US-186568P.  
 PR 14-MAR-2000: 2000US-189320P.  
 PR 14-MAR-2000: 2000US-189328P.  
 PR 15-MAR-2000: 2000W0-US06884.  
 PR 21-MAR-2000: 2000US-190828P.  
 PR 21-MAR-2000: 2000US-191007P.  
 PR 21-MAR-2000: 2000US-191048P.  
 PR 21-MAR-2000: 2000US-191314P.  
 PR 28-MAR-2000: 2000US-192555P.  
 PR 29-MAR-2000: 2000US-193032P.  
 PR 29-MAR-2000: 2000US-193033P.  
 PR 30-MAR-2000: 2000W0-US08439.  
 PR 04-APR-2000: 2000US-194449P.  
 PR 04-APR-2000: 2000US-194547P.  
 PR 11-APR-2000: 2000US-195975P.  
 PR 11-APR-2000: 2000US-196000P.  
 PR 11-APR-2000: 2000US-196187P.  
 PR 11-APR-2000: 2000US-196590P.  
 PR 11-APR-2000: 2000US-196820P.  
 PR 18-APR-2000: 2000US-198121P.  
 PR 18-APR-2000: 2000US-198585P.  
 PR 25-APR-2000: 2000US-199397P.  
 PR 25-APR-2000: 2000US-199550P.  
 PR 25-APR-2000: 2000US-199654P.  
 PR 03-MAY-2000: 2000US-201515P.  
 PR 17-MAY-2000: 2000W0-US13705.  
 PR 22-MAY-2000: 2000W0-US14042.  
 PR 30-MAY-2000: 2000W0-US14941.  
 PR 02-JUN-2000: 2000W0-US15264.  
 PR 05-JUN-2000: 2000US-205832P.  
 PR 28-JUL-2000: 2000W0-US20710.  
 PR 22-AUG-2000: 2000US-064484P.  
 PR 24-AUG-2000: 2000W0-US23328.  
 PR 08-NOV-2000: 2000W0-US30952.  
 PR 01-DEC-2000: 2000W0-US32678.  
 PR 20-DEC-2000: 2000W0-US34956.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL:  
 PI Fan J, Smith V, Watanabe CK, Wood WI, Zhang Z:  
 XX  
 DR WPI: 2001-602746/68.  
 DR N-PSDB: AAS45964.  
 XX  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumours, such as prostate and breast tumours, in mammals and  
 PT to screen for modulators of the compounds -  
 XX  
 PS Claim 11: Fig 80: 774pp: English.  
 XX  
 CC Sequences AAM29024-AAM29428 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, rats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO

CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders.  
 XX  
 XX  
 SC Sequence #1 AA:  
 Query Match: 11.44 Score 810 Db 22 Length 611  
 Best Local Similarity 44.84: Fred, No. 2, 1e-75  
 Matches 161: Conservative 55: Mismatches 124: Gaps 20: Gaps 4:  
 QY 14 TLGLALPALPAIAANSSRRMGVAVYASSINILDSLSLVVYIPSLJLSRKQRLPIR 73  
 Db 9 SLRLVAVFSMAASN-----WLYIAKLSVSGSISEETGE-----KIKLLQPLQWCK 58  
 QY 74 ONPGTSSVSGSLQSVARECKQKQFRRNRNCPVAGPHLPKRVNCPRETAFAITSA 133  
 Db 59 KRLVKSIVRGGQALAECCQGFRRNRNCGTSLSLVPRKVVY23:REAAVYAISSA 118  
 QY 134 GYTHSVARSCBSLESTCIRRRGGGQPDHWGSCSNDITFLFGREFVSGEGR- 192  
 Db 119 GVAFVTRKSSGDELKCCGCRIVAVSPQGFQWSSCSNIAVVAESQFVDVERSKG 178  
 QY 139 --ELPELMINNEEAFFITVESENKCECKCHMSGSGCTVRIWWR-PLTAVGDLPRPF 250  
 Db 179 ASSSALMNINNEFAKRAILTHRVCKCHGVSSCEVKIWKAVPFRQYHALKEKF 238  
 QY 251 DQASVAVYGRNSNFAKRELLRLPEPDAKRPSPHDLVTHKSTVFYVSGRIGTGT 310  
 Db 239 GAAVVEPRVYSSFA-----LVFKNAGFKHDEEDLVTHKSTVFYVSGRIGTGT 291  
 QY 311 ANKAVNSSSPALDQFELDQNRHRIKPGVTEKQNCITRWVYVSFNTIPIVLEHC 369  
 Db 292 KRLT NKTSTKAMIGLELDTNPFHIAQVETAEKSCKEHWVYVY292:PLVELHTG 350  
 RESULT 13  
 ID AAM38889 standard: protein: 651 AA.  
 XX  
 AC AAM38889:  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID No 2014.  
 XX  
 KW Human: isotropic; immunosuppressant; cytostatic; bone therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemoplastic;  
 KW chemokinesis; thrombolytic drug screening; arthritis; inflammation;  
 KW leukaemia  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200153472-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000: 2000W0-US34264.  
 XX  
 PR 21-JAN-2000: 2000US-048872P.  
 PR 25-APR-2000: 2000US-055231P.  
 PR 09-JUL-2000: 2000US-058604P.  
 PR 19-JUL-2000: 2000US-062031P.  
 PR 03-AUG-2000: 2000US-0653450.  
 PR 14-SEP-2000: 2000US-066219P.  
 PR 19-OCT-2000: 2000US-0693074.  
 PR 29-NOV-2000: 2000US-072734P.  
 XX  
 PA (HFE-) HESCO INC.  
 XX

KM		amyotrophic lateral sclerosis; Shy-Drager Syndrome; thrombotic;
KL		chemokine; chemokine; chemokine; chemokine; chemokine; chemokine;
KW		leukemia.
XX		Homo sapiens.
XX		WZ000153312-A1.
P9	26-JUL-2001.	
FR	26-DEC-2000; 2C6BW-US-1283.	
FR	21-JAN-2000; 2000US-046725.	
FR	25-APR-2000; 2000US-052313.	
PR	09-JUL-2000; 2000US-052312.	
PR	19-JUL-2000; 2000US-052312.	
PR	01-NOV-2000; 2000US-065450.	
PR	14-SEP-2000; 2000US-065450.	
PR	14-OCT-2000; 2000US-065450.	
PR	29-NOV-2000; 2000US-072344.	
XX		(HSE-) HSDG INC.
PA		Tanaka Y., Liu C., Asundi V., Chen P., Ma Y., Qian X., Ren F., Wang D.,
P1	Mang J., Wang Z., Weinman J., Xu C., Xue A., Yang Y., Zhang J.,	
P1	Zhao Q., Zhou F., Goodrich R., Dimasac RT.	
XX		WPI: 2001-44253/47.
OR	N-PDBI: AAI59831.	
XX		Novel nucleic acids and polypeptides, useful for treating disorders
P7	such as central nervous system injuries -	
P7		Example 2: SEQ ID NO 5606; 1007APP; English.
PS		The invention relates to human nucleic acids (AA1577-e-AA1399) and
CC		the encoded polypeptides (AA13842-AA4213) with neurotropic,
CC		immunopressant and cytostatic activity. The polynucleotides are useful
CC		in gene therapy. A composition containing a polypeptide or polynucleotide
CC		of the invention may be used to treat diseases of the peripheral nervous
CC		system, such as peripheral nervous injuries, peripheral neuropathy and
CC		localized neuropathies and central nervous system diseases, such as
CC		Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC		lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC		utilization of the activities such as: immune system suppression,
CC		activation/inhibit activity, chemotactic/chemokinetic activity, haemostatic
CC		and thrombolytic activity, cancer diagnosis and therapy drug screening,
CC		assays for receptor activity, arthritis and inflammation, leukemias and
C2		C.N.S. disorders.
C2		Note: The sequence data for this patent did not form part of the printed
C2		specification.
S2	Sequence 365 AA:	
QY	Query Match 41 % Score 840 DB 22 Length 365	
QY	Best Local Similarity 44.8% Pred No. 2.2e-75	
QY	Matches 151 Conservative 55 Mismatches 123 In gaps 20 Gaps 4	
QY	14 TLLAALTAALFAALANSNHWGIIVAVASSTNLITDSKSLQLLEHSLGLSRKQRLLR 73	
QY	23 SLRLVAFAVASAASN-----WLTKAKLSVSISSEETCE-----KRIKIQOVGMCK 72	
QY	74 QNPGLHSVSGSLOSVDKWKPFNNMNCTAGPDLGRKTVNGTETAFATISA 133	
QY	73 RLTEVMSVRHQALAEQQCYCPFMNMGNSLTDSLPLPGKVTLIGLRKAPFAYIASA 132	
QY	134 GVTSHSVARSSESIESICTCYRRKGIGRPDMHGCGSDNDIRGLFJHELVDSGEKR- 192	
QY	134 GARFNVTRASSSELKKGGCDRTVHVSPQGOWMSGSDNIAGVAFCSFDVDFERSKG 192	
QY	193 -----ELRFMLLNHNKAGKTIVSEMROECCHRGSSQCTVCIMKRLTFEAVGVLRDRF 250	
QY	194 ASSSAALMLNHNEGKRAILLTHKEPCCHGVSSCEVTCFARVFPE-VSHALKERF 252	





GenCore version 5.1.4.P5.4578  
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# OM protein - protein search, using sw model

Run on: April 22, 2003, 16:38:38 : Search time 30 seconds  
(without alignments) 362.993 Million cell updates/sec

Title: US-09-674-292-1  
Perfect score: 2036  
Sequence: 1 MGLWALPGWVSATLLLA.....WGVNPNMTHTVRLHCL 370

Scoring table: BLAST62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 462574

Minimum DB seq length: 9  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA\*  
1: /cgn2.6/ptodata/1/aa/5A.COMB.pep.\*  
2: /cgn2.6/ptodata/1/aa/5B.COMB.pep.\*  
3: /cgn2.6/ptodata/1/aa/5A.COMB.pep.\*  
4: /cgn2.6/ptodata/1/aa/5B.COMB.pep.\*  
5: /cgn2.6/ptodata/1/aa/PTCTS.COMB.pep.\*  
6: /cgn2.6/ptodata/1/aa/BACKFILE1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	840.5	41.3	355	3	US-09-082-270-2
2	834	41.0	351	4	US-09-067-782A-2
3	756	37.1	397	1	US-08-647-928-B
4	731.5	35.3	372	3	US-09-082-089-2
5	723.5	35.5	359	3	US-09-082-089-3
6	723.5	35.5	363	3	US-09-082-089-5
7	720.5	35.4	349	4	US-09-439-774-2
8	709.5	34.8	389	2	US-08-485-449-2
9	709.5	34.8	389	2	US-08-485-449-7
10	707	34.7	389	2	US-08-485-449-6
11	679	33.3	376	2	US-08-485-449-5
12	373.5	18.3	159	3	US-09-082-270-4
13	336.5	16.5	121	4	US-09-067-782A-5
14	225	11.1	131	4	US-09-067-782A-4
15	113.5	5.6	115	2	US-08-485-449-4
16	99	4.9	956	1	US-08-185-232A-2
17	99	4.9	956	1	US-08-416-523-2
18	99	4.9	956	3	US-08-789-478-2
19	96	4.7	399	4	US-09-553-498-2
20	96	4.7	399	4	US-09-618-869-2
21	91	4.5	519	4	US-09-211-794A-7
22	89.5	4.4	1652	4	US-09-627-650B-1
23	89.5	4.4	1652	4	US-09-436-063C-1
24	89.5	4.4	1617	4	US-09-627-650B-5
25	89.5	4.4	1917	4	US-09-436-063C-5
26	89.5	4.4	2508	4	US-09-627-650B-7
27	89.5	4.4	2508	4	US-09-436-063C-7

28	89.5	4.4	4544	4	US-09-627-650B-3	Sequence 3, Appl 1
29	89.5	4.4	2544	4	US-09-436-063C-3	Sequence 3, Appl 1
30	89.5	4.4	2601	4	US-09-627-650B-9	Sequence 9, Appl 1
31	89.5	4.4	2601	4	US-09-436-063C-9	Sequence 9, Appl 1
32	89.5	4.4	605	1	US-08-152-019A-26	Sequence 26, Appl 1
33	89.5	4.4	605	3	US-08-482-677-4	Sequence 4, Appl 1
34	89.5	4.4	605	4	US-08-650-599A-1	Sequence 1, Appl 1
35	89.5	4.4	605	4	US-09-490-517-1	Sequence 22, Appl 1
36	89.5	4.4	606	3	US-08-665-255-22	Sequence 9, Appl 1
37	89.5	4.4	606	4	US-08-762-500-22	Sequence 9, Appl 1
38	89.5	4.4	606	4	US-09-306-902A-9	Sequence 40, Appl 1
39	89.5	4.4	749	1	US-08-454-455-6	Sequence 3, Appl 1
40	88.5	4.3	529	1	US-08-152-019A-4	Sequence 3, Appl 1
41	88.5	4.3	529	3	US-08-650-599A-3	Sequence 2, Appl 1
42	88.5	4.3	529	4	US-09-490-517-3	Sequence 2, Appl 1
43	88.5	4.3	604	2	US-08-635-137-2	Sequence 17, Appl 1
44	88.5	4.3	604	4	US-09-136-981-2	
45	88.5	4.3	4556	1	US-08-185-432-17	

## ALIGNMENTS

RESULT 1  
US-09-082-270-2  
Sequence 2, Application US/09082270  
Patent No. 6043053  
GENERAL INFORMATION:  
APPLICANT: BARNES, MICHAEL  
APPLICANT: TESTA, TANIA  
TITLE OF INVENTION: NO. 6043053el Compounds  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FATHER S. PRESTIA  
STREET: P.O. BOX 980  
CITY: VALLEY FORGE  
STATE: PA  
COUNTRY: USA  
ZIP: 19482  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSU for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/082,270  
FILING DATE: 20-MAY-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 970716.3  
FILING DATE: 23-MAY-1997  
APPLICATION NUMBER: GB 9804921.6  
FILING DATE: 06-MAR-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F.  
REGISTRATION NUMBER: 23-0341  
REFERENCE/CITATION NUMBER: GB-90164  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0705  
TELEFAX: 610-407-0702  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-082-270-2  
Query Match 41.3% Score 840.5 DB ID Length 3553  
Best Local Similarity 46.0% Pred. No. 1.4e-77  
Matches 155: Conservative 52: Mismatches 12: Indels 9: Gaps 3:

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QY 34 MWGIYVNASSTNLLTDSKSLQVLEPSSLQSKORRLKQNPGLHSVSGLSQSAVREC 93
DB 26 MWSLAQGVYLSL-----GSPDLGSGIPOLYKQLRRCRNITLIMPSVAEYKGLIDEC 80
QY 94 KWQFNRRMWKPTAPGP-HLEFGKIVNRCRETAIFAIFAITSGVTHSVARSCSGSIEST 152
DB 81 QHOFGRKMKCTTIDISLALFQPVLDKATRESAFVAHAIASGVAFAVTRSCAGISTIQ 146
QY 153 QCYRRRGPGVDPWHWGGCSDNIDFGRLGHEPEYDSSEKPOLRFLMLHNHAGRTYVS 212
DB 141 CDSHHKCPGPGGKWKGGCSGSDADGCVLYSEFADAHENRPARSANKKHNEAGRTITL 200
QY 213 EMKQPCGHMSGCTVPTCKMLPTLRVAVDYLKCFEDVASRVLYNKGNSKNSAEIL 272
DB 201 HHMLCKCKGHLSGCTEVKTCWMAQPDFRAIGDLKIKTISASENVV---EKHRESKWE 257
QY 273 RLEEDPAHKKPSPHLYVEFEKSPNCTVYSGFLGTAGASACSSSPALNGLLQCGR 332
DB 258 TLRAKYSLLKPTERDLYVENSNPCEPNETGSPTRDKCNVTSHGIDGDLQGR 317
QY 333 GHRITQVTERCNCITFKGCHVSCRNITIRVLEEC 369
318 GHNTRTERKREKCHIFHWGCVYSGQCFIRIVVHIC 354

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## RESULT 2

```

US-09-067-782A-2
: Sequence 2, Application US/09067782A
: Patent No. 6165751
: GENERAL INFORMATION:
: APPLICANT: BARNES, MICHAEL
: TITLE OF INVENTION: NOVEL COMPOUNDS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Patner & Prestia
: STREET: P.O. Box 960
: CITY: Valley Forge
: STATE: PA
: COUNTRY: US
: ZIP: 19482-0960
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: IBM Compatible
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/067,782A
: FILING DATE: 28-APR-1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: UK 9710744.6
: FILING DATE: 23-MAY-1997
: APPLICATION NUMBER: EP 9730944.0
: FILING DATE: 13-MAY-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Prestia, Paul F
: REGISTRATION NUMBER: 23,031
: REFERENCE/DOCKET NUMBER: GH-30167
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 601-407-0790
: TELEFAX: 610-407-0751
: TELEX: 846169
: INFORMATION FOR SEQ. ID NO.: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 351 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-067-782A-2

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Query Match 41.0% Score 831: Db 4: Length 351:

Best Local Similarity 44.4% Pred. No. 6,3e-77: Matches 1607 Conservative 557 Mismatches 1241 Incons 20 Gaps 4:

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QY 14 TLLALAAEPALANSSGRWGIYVNASSTNLLTDSKSLQVLEPSSLQSKORRLIR 73
DB 9 STRLIVAVFSAASN-----WLYAKLSVGSISEETCE-----KELIIGQVQMK 58
QY 74 QNPGLHSVSGLSQSAVECKWQFNRNRCPTAPRPLTGKIVNRCRETAIFAIFAITSA 133
DB 59 KLEVMISVNRKQGLAIEEVOYFRNKNQSTLDSLIVQKVTI--GLEALYATLSA 116
QY 134 GYTHSVARSCSGSIESCTDYRRRGSGPDMHWGGCSDNIDFGRLGHEPEYDSSEGR 192
DB 119 GVAFVTHACSSSELEKCCDEKTVHGVSPQGFOWSGSDNIAYVAFSSVQVRSKG 178
QY 193 --DREFIMLNHNHAGRTYVSEKQPCGHMSGCTVPTCKMLPTLRVAVDYLKCFE 250
DB 193 ASSPAMLNHNHAGRAILTHKWECKGHVSSGCTEVKTCWMAQPDFRAIGDLKIK 238
QY 251 DGASRVLYNKGNSKNSAEILLREEDPAHKKPSPHLYVEFEKSPNCTVYSGRLTAG 310
DB 239 LGATEVEFFPVGSSRA-----LVPRNAQFPHTDELYLEPSNPGGLTMSVYIGT 241
QY 311 AGRANSSPALDQGLDQGRGHRITQVTERCNCITFKGCHVSCRNITIRVLEEC 369
DB 292 KRTCNKTSKALINSGELDQGRGHITAOVELAKRSCGFHWGCVYSGQCFIRIVVHIC 350

```

## RESULT 3

```

US-08-647-928-8
: Sequence 8, Application US/08647928
: Patent No. 578-421
: GENERAL INFORMATION:
: APPLICANT: Kodan, Gideon A.
: APPLICANT: Parledge, Sue Jane
: APPLICANT: Schmidt, Arzel
: TITLE OF INVENTION: DNA ENCODING THE WNT-X GROWTH FACTOR
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: John W. Wallen
: STREET: 126 E. Lincoln Avenue
: CITY: Rahway
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07065
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent in release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/647,928
: FILING DATE: 22-MAY-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/172,365
: FILING DATE: 22-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Wallen, John W.
: REGISTRATION NUMBER: 45,473
: REFERENCE/DOCKET NUMBER: 19-16
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (908) 594-3905
: TELEFAX: (908) 594-4720
: INFORMATION FOR SEQ. ID NO.: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 397 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-647-928-8

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Wed Apr 23 07:41:00 2003

us-09-674-292-1.ra1

Page 4

FILING DATE: 25-FEB-1998  
APPLICATION NUMBER: GR 9804007.4  
FILING DATE: 25-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F.  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-30166  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-082-089-3

Query Match 35.5% Score 723.5; DB 3; Length 359;  
Best Local Similarity 39.0%; Pred. No. 1,20-65;  
Matches 142; Conservative 65; Mismatches 222; Indels 35; Gaps 7;

15 LLLALLAPALA-----ANSSGRWYIVNASSNILLITSSKGLVLEP---STGLLSR 66  
1 LLLFTALSSWAQLITDANS--WMSL-----ALNVPQPEMTTGAQPVTSJLPGLSP 56  
67 KQRLIPQNGILHSVSGLOSAYVECKQGFNPRKMPPTAPSPHLKIVNRJTTETAF 126  
57 GQRLCQIVQHMAYTEGAKTIKQCGQFPQPRKSTINQASVFSVWJLSRETAIF 116  
127 IFATISGTHSVASCSSESIESCQDVRFRGQSP-DEWVSGSDNTHPKLGEPEV 185  
117 THAVSAGVYVNAISPAQSECELSLQGSRTAPKPLEPDWVNRSDQINREYVFAKEV 176  
186 DSDEKREL-----PFLNLIHNEAGRTVESEMKQDCKTHMSNSQIVRTWMELP 237  
177 DAREERKNIAKSGEEQGVNLNLDNNAGRAVYKMAVNAKQVCSKCRKTIWGLA 236  
278 TLRAVGVLDREPDGASVLYGNQSNRASRAELLKLEPEHPARKPSPHILVYFEKSN 297  
477 EFRAVGVLRKREKYSAAARVTRKQ-----KLELVNSRTQPTFDILVYVDSFD 286  
298 FCTYSGRLTAGTAGACNSSSPALDQCELLQCGGKHTKQVYTERNCITWMCCHVSQ 357  
287 YCLNNESTDSLTGRLCNKTSQDMQCEIMQSGGYNQKSVQVCHCKTHWQCFVKG 346  
358 KNT 451  
347 KKT 350

RESULT 6  
US-09-082-089-5  
Sequence 5, Application US/09082089  
Patent No. 6109960  
GENERAL INFORMATION:  
APPLICANT: BARNES, MICHAEL  
APPLICANT: PRESTIA, TANIA  
APPLICANT: KESTEL, DAVID  
TITLE OF INVENTION: NO. 6100696el Compounds  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATNER & PRESTIA  
STREET: P.O. BOX 980  
CITY: VALLEY Forge  
STATE: PA  
COUNTRY: USA  
ZIP: 19462  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/674-292-089  
FILING DATE: 20-MAY-1998  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 970737.9  
FILING DATE: 23-MAY-1997  
APPLICATION NUMBER: GB 9803921.1  
FILING DATE: 25-FEB-1998  
APPLICATION NUMBER: GB 9804007.4  
FILING DATE: 25-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: PRESTIA, PAUL F.  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: GH-30166  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 453 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-082-089-5

Query Match 35.5% Score 742.5; DB 3; Length 453;  
Best Local Similarity 39.0%; Pred. No. 1,20-65;  
Matches 142; Conservative 65; Mismatches 122; Indels 35; Gaps 7;

15 LLLALLAPALA-----ANSSGRWYIVNASSNILLITSSKGLVLEP---STGLLSR 66  
1 LLLFTALSSWAQLITDANS--WMSL-----ALNVPQPEMTTGAQPVTSJLPGLSP 56  
67 KQRLIPQNGILHSVSGLOSAYVECKQGFNPRKMPPTAPSPHLKIVNRJTTETAF 126  
57 GQRLCQIVQHMAYTEGAKTIKQCGQFPQPRKSTINQASVFSVWJLSRETAIF 116  
127 IFATISGTHSVASCSSESIESCQDVRFRGQSP-DEWVSGSDNTHPKLGEPEV 185  
117 THAVSAGVYVNAISPAQSECELSLQGSRTAPKPLEPDWVNRSDQINREYVFAKEV 176  
186 DSDEKREL-----PFLNLIHNEAGRTVESEMKQDCKTHMSNSQIVRTWMELP 237  
177 DAREERKNIAKSGEEQGVNLNLDNNAGRAVYKMAVNAKQVCSKCRKTIWGLA 236  
278 TLRAVGVLDREPDGASVLYGNQSNRASRAELLKLEPEHPARKPSPHILVYFEKSN 297  
477 EFRAVGVLRKREKYSAAARVTRKQ-----KLELVNSRTQPTFDILVYVDSFD 286  
298 FCTYSGRLTAGTAGACNSSSPALDQCELLQCGGKHTKQVYTERNCITWMCCHVSQ 357  
287 YCLNNESTDSLTGRLCNKTSQDMQCEIMQSGGYNQKSVQVCHCKTHWQCFVKG 346  
358 KNT 451  
347 KKT 350

RESULT 7  
US-09-459-774-2  
Sequence 2, Application US/09459774  
Patent No. 6207040  
GENERAL INFORMATION:  
APPLICANT: Michael Robert Barnes  
APPLICANT: Tania Tamson Prestia  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP-30193  
CURRENT APPLICATION NUMBER: US/09/459,774







TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELE: 706141  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 389 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

Query Match 34.8%; Score 709.5; DB 2; Length 389;  
 Best Local Similarity 38.5%; Pred. No. 3, 7e-64;  
 Matches 153; Conservative 53; Mismatches 122; Indels 69; Gaps 10;

QY 23 PALAANSGRWGVVWVASTNLTDLS-KSLQVLEP-----STQLLSKRRRLI 72  
 DB 11 PSCLA-----GLLEFLALCSKALSNELSLKLEDFPLTNTVCLTSLGSKRQLD 62  
 QY 73 RQNPGLHVSQGLQSAVRECKWQFNKRWNPITAPG---PHLEKIVNRCETAFIF 128  
 DB 63 LRNPDTASALQGLHIAVHECQHQHLDQRWNCALBQGRLEPH-HSAILKGFESAFSP 121  
 DB 129 AITSASVTHSVARSSEGSLESCDYARRG----- 159  
 DB 122 SMLAGVMAVAITAGSIAKLVSQGGKMSGEQHLPAKLILQDALSRKSFPSLESP 181  
 QY 160 -----PSSKQ-WHMGSTNINIDFRLPREFVESERDELFLMNLNNEARCTVVS 272  
 DB 182 PSSSPFGVPTWMOGQCNHMDFSKTSRFDLSKRAHPDIYAHMRINHRVRYVTH 241  
 QY 213 EMQERKTRMSASCTVPTNMLEFLIYAGDVLPFEDASVYANGN-SNARSRELL 272  
 DB 412 NLRKKKCHTISQSCFKRTWAPAFRAGALRELP--GRAIFDT-HNRNSGAPQ 297  
 QY 273 RLEPEDPAKRPSPHDLVYEFKSPNCTYSRLQTAITASRAVNSSSPALDQCELLCG 342  
 DB 298 RLPRRLS-----GELYEFKSPDCEPDPTMSPTSRANITSRLDQCSLQCSH 351  
 QY 333 GHRTPTQVIFPCNCTFHWCHVSCNCTHTRVLEHC 369  
 DB 352 GHNVLQPTVERCHCRHRCWQVYLCEKVELEWNVV 389

RESULT 10  
 US-08-485-449-6  
 : Sequence 6, Application US/08485449  
 : Patent No. 5824789  
 : GENERAL INFORMATION:  
 : APPLICANT: VANDENBERG, DAVID  
 : TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE  
 : TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE  
 : NUMBER OF SEQUENCES: 7  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: MARRISON & FOSTER  
 : STREET: 755 Page Mill Road  
 : CITY: Palo Alto  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 94304-1018  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.00  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/485,449  
 : FILING DATE:  
 : CLASSIFICATION: 536  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: KONSKI, ANTOINETTE F.  
 : REGISTRATION NUMBER: 34,202

REFERENCE/DOCKET NUMBER: 20296-20035,00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELE: 706141  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 489 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

Query Match 34.7%; Score 707; DB 2; Length 389;  
 Best Local Similarity 39.6%; Pred. No. 6, 6e-64;  
 Matches 149; Conservative 48; Mismatches 119; Indels 60; Gaps 8;

QY 43 STMLILRSKSLVLEP-----STQLLSKRRRLIRQPGGTHVSGTQSAVREG 73  
 DB 24 SRALSNEILGKLGDEPLTANTVCLTSLGSKRQLDLSRFLVTSALQGLHIAVHEC 83  
 QY 94 KWFPRKRNPTAPG---PHLEKIVNRCETAFIFAITSAVHVSARSSEGSYE 149  
 DB 84 QHQLKCPWNSALEBQGRLEPH-HSAILKGFESAFSPMLAAVMAVAITAGSKLV 142  
 QY 150 SCTQVYRRG----- 173  
 DB 14 SCQCNKRSQDQSLAKLLQDALSRKIFPSSQSPVSSVSPHCTWMOGQCNH 202  
 QY 174 IDFGRLPRKEVINSGEKRLFLMNLNNEARCTVSEMDQEK-HDSGNTVYETQW 233  
 DB 2 SCQGNKSHEDLSREAFPLIYAHMRINHRVRYVTEMLERK-KHYSQSCFKRTW 262  
 QY 234 MRPLTAVAGDVLPFEDASVLYLGNRGSNARSRAELRLLELPAPKRPSPHDLVYEP 293  
 DB 263 RAAPFERAIGALRELP--SRAIFDT-HNRNSGAPQRLPRRLS 312  
 QY 294 KSPNCTISQGLTAGAGACVNSSSPALDQCELLCGSGHTRVYVTEKNCITHWGC 353  
 DB 413 KSPDTEPDPLSGPTGRACNKTISRLDQCSLQCSGHNVVLQPTVERCHCRHRCW 372  
 QY 454 HVSRCNCTHTRVLEHC 369  
 DB 473 YVLCEKVELEWNVV 389

RESULT 11  
 US-08-485-449-5  
 : Sequence 5, Application US/08485449  
 : Patent No. 5824789  
 : GENERAL INFORMATION:  
 : APPLICANT: VANDENBERG, DAVID  
 : TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE  
 : TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE  
 : NUMBER OF SEQUENCES: 7  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: MARRISON & FOSTER  
 : STREET: 755 Page Mill Road  
 : CITY: Palo Alto  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 94304-1018  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/485,449  
 : FILING DATE:  
 : CLASSIFICATION: 536  
 : ATTORNEY/AGENT INFORMATION:

```

: NAME: KONSKI, ANTOINETTE F.
: REGISTRATION NUMBER: 34,202
: REFERENCE/DOCKET NUMBER: 20296-20035.00
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 376 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-485-449-5

Query Match          33.3% Score 679; DB 2; Length 376;
Best Local Similarity 39.5%; Pred. No. 4,5e-61;
Matches 149; Conservative 49; Mismatches 121; Indels 58; Gaps 11;

: 36 GIVNASSNLLTDSKSLQVLEP-----SLQLSKRQRLINQNGIHSVSLQ 87
: 14 GLFLALSRALSNETILGKIPGEPLINTVCLTSLSKRQDQLCLP-EDVTASALQ2LH 72
: 88 SAVCECKWQFRRRNQCTAPG---PHLEGRVNRGGRFAIFAITAGVTHSVASG 143
: 73 IAVHEDQHLPQRMNCSALEGGRLPH-HSALIKGRFRESAFSFMLAGVMAVATAG 131
: 14 SEGSIESCTGCTRRRG-----PGSPD-----WHMGGSID 172
: 132 SLGLVNGCGWKGSGEDRLAKLLQLQLALSQKFPSPSPSPSPGQDITWEGGNH 191
: 173 NIDGRLLFGREFYDSGEKGRDLRLKLNHNNEAGRTVFSEMRQECKGMSGCVTVC 232
: 192 DMDEGEKFSRDLDSREAPRDIOARMHNHNVGQVVTENLKRKCKGCTGSGCFKTC 251
: 233 WMRPLTRAVGVLKDRFDGASRYLYGNSGSKRASRALLLLEPHFAKRPSPHDIYF 292
: 252 WRAAPERRA-GALPERL---RAIFLDT-HNNNGAHPRLRRLS-----SELYVF 295
: 293 EKSPNEFYSGRLGTAGTACGACGSSPALDQGLCCGRSHRTPTQVTEKCNCTFFMG 352
: 300 EKSPDICE-RDPTGSHGTGRACKTKSLIDNGSLCCGRSHNYLQTVTEKCHREFMG 358
: 353 CHVSCFNCITRYLHEC 369
: 359 CYVLDECKYTERWNVG 375

RESULT 12
US-09-082-270-4
: Sequence 4, Application US/09082270
: Patent No. 6043053
: GENERAL INFORMATION:
: APPLICANT: BARNES, MICHAEL
: APPLICANT: TESTA, TANIA
: TITLE OF INVENTION: No. 6043053el Compounds
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: RATHER & PRESTIA
: STREET: P.O. BOX 980
: CITY: VALLEY Forge
: STATE: PA
: COUNTRY: USA
: ZIP: 19442
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSU for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/082,270
: FILING DATE: 20-MAY-1998
: CLASSIFICATION:

```

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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9710716.3
: FILING DATE: 23-MAY-1997
: APPLICATION NUMBER: GB 9604921.6
: FILING DATE: 06-MAY-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: PRESTIA, PAUL F.
: REGISTRATION NUMBER: 23,031
: REFERENCE/DOCKET NUMBER: GB-30164
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-407-0700
: TELEFAX: 610-407-0701
: TELEX: 843159
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 159 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-082-270-4

Query Match          34.3% Score 373.5; DB 2; Length 159;
Best Local Similarity 44.0%; Pred. No. 2.1e-73;
Matches 71; Conservative 19; Mismatches 54; Indels 5; Gaps 1;

: 106 IANGPHLEKRIYNRQDETAIFAITSAGVTHSVARSGSGESIESITCYRHPKQSGSPW 165
: 8 SVTEHFL-----NATPSSAFVMAIASAVATPSCACETISITCTSSHHKFFPEEM 62
: 106 HW31NDIDEFPLFGREFYDSGEKGRDLRLKLNHNNEAGRTVFSEKPEQYKCHKMSG 225
: 63 KWD3SELDADFGVLYGVGADARENPPDARSAMKHNNEAKTITLCHWHLCKCFHLSG 122
: 226 SCATYTCMRPLTPLAVTDVLRDFDGA 253
: 123 SPEKRTWMAJERHAIQDFLKKIKYSA 150

RESULT 13
US-09-067-782A-5
: Sequence 5, Application US/09067782A
: Patent No. 6105761
: GENERAL INFORMATION:
: APPLICANT: BARNES, MICHAEL
: TITLE OF INVENTION: NOVEL COMPOUNDS
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Rather & Prestia
: STREET: P.O. BOX 980
: CITY: Valley Forge
: STATE: PA
: COUNTRY: US
: ZIP: 19442-0980
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSU for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/067,782A
: FILING DATE: 28-APR-1998
: CLASSIFICATION: 445
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: UK 9710734.6
: FILING DATE: 23-MAY-1997
: APPLICATION NUMBER: EP 97309144.0
: FILING DATE: 14-N-V-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Prestia, Paul F.
: REGISTRATION NUMBER: 23,031
: REFERENCE/DOCKET NUMBER: GB-30157
: TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 601-407-0700  
 TELEFAX: 610-407-0701  
 TELEX: 846169  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 121 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-067-782A-5

Query Match 16.5% Score 395.5; DB 4; Length 121;  
 Best Local Similarity 48.8%; Pred. No. 6,44e-27;  
 Matches 62; Conservative 12; Mismatches 46; Indels 7; Gaps 11

QY 243 GDLVLRHVGASRVLYGNKGSNFKASFAELMLLEPHDPAHKPPSPHDIVYEFKSPNETYS 402  
 D6 1 GHALKKEKHGATVEPERVYSSHA-----LVFNQKPEPHIDELVLYEPSPDEQC 53  
 QY 303 GRIGTAGTASACNSSSPALDGCGLCGRGHRTFLVTERENCTFHWOCVAGNCTH 362  
 D6 54 MRGVLTIRGTRFKRKISKALDGCGLCGRGHIAVYELAEKRSKRFHWOCVACROQAR 113  
 QY 363 TRVLHBC 669  
 D6 114 LVELHTG 120

RESULT 14  
 US-09-067-782A-4  
 Sequence 4, Application US/09067782A  
 Patent No. 6163751  
 GENERAL INFORMATION:  
 APPLICANT: BARNES, MICHAEL  
 TITLE OF INVENTION: NOVEL COMPOUNDS  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Palmer & Prestia  
 STREET: P.O. Box 980  
 CITY: Valley Forge  
 STATE: PA  
 COUNTRY: US  
 ZIP: 19482-0980  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/067,782A  
 FILING DATE: 28-APR-1998  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: UK 9710734.6  
 FILING DATE: 23-MAY-1997  
 APPLICATION NUMBER: EP 97309144.0  
 FILING DATE: 13-NOV-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Prestia, Paul F  
 REGISTRATION NUMBER: 23,031  
 REFERENCE/DOCKET NUMBER: GH-30167  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 601-407-0700  
 TELEFAX: 610-407-0701  
 TELEX: 846169  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 131 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-09-067-782A-4  
 Query Match 11.1% Score 225; DB 4; Length 131;  
 Best Local Similarity 36.8%; Pred. No. 2.3e-15;  
 Matches 49; Conservative 32; Mismatches 42; Indels 10; Gaps 2

QY 14 TLILAALPALANSSGRWGIYVASSNTLITDSKSLQVLEFPELGLSKRKRRLR 73  
 D6 4 SRLLYFAVFSAASN-----MLYLAKSSVGSISEEICE-----KGLGIDQVQMK 56  
 QY 74 QNPGILHSVSGLSAVHECKMFRFRMNCPAPRPHLEGVNPRFEPAFPAITSA 133  
 D6 59 RNLVEMSEVFGAQLAIEHQVQFRRKMNCSITLSELVFRKVVYLTPEPAFVAMISA 118  
 QY 134 GVTHSARCSHG 146  
 D6 119 GVCFAVTRPQNSG 131

RESULT 15  
 US-08-485-449-4  
 Sequence 4, Application US/08485449  
 Patent No. 5624789  
 GENERAL INFORMATION:  
 APPLICANT: VANDERBERG, LAYD  
 TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE  
 TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-5018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy Disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/485,449  
 FILING DATE:  
 CLASSIFICATION: 5,6  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOSKIS, ANTOINETTE E  
 REGISTRATION NUMBER: 34,282  
 REFERENCE/DOCKET NUMBER: 20206-20035, 09  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 115 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-485-449-4

Query Match 5.6% Score 113.5; DB 2; Length 115;  
 Best Local Similarity 32.1%; Pred. No. 0.00045;  
 Matches 36; Conservative 17; Mismatches 36; Indels 23; Gaps 5

QY 43 AALANSSGRWGIYVASSNTLITDS-KSLQVLEF-----SRLSRQRRLI 72  
 D6 11 PSGLA-----GLFLALCSRLSNELIGLKGPEPLTGNVTCLTSLSGSKQGLG 62  
 QY 74 KNPGLHSVSGLSAVHECKMFRFRMNCPAPRPHLEGVNPRFEPAFPAITSA 120  
 D6 63 LNPDTVASALQGLIAVHECQHLRQWNCSALEGGGRLEFH-HSALTKRG 113

Wed Apr 23 07:41:00 2003

us-09-674-292-1.ra1

Page 9

Search completed: April 22, 2003, 16:42:57  
Job time : 37 secs

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GenCore version 5.1.4\_p5\_457d  
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(without alignments)  
1482.401 Million cell updates/sec

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Perfect score: 2036  
Sequence: 1 MGIMALLPGWVSATILLALA.....WGVHVSCHNCITHTVLEEL 370

Scoring table: HLOSDM62  
Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues  
Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
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2: /cgn2\_6/ptodata/1/pubppa/PT1\_NEW\_PUB pep:\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB pep:\*  
4: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB pep:\*  
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9: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB pep:\*  
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14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	ID	Description
1	840	41.3	351	US-09-978-295A-226	Sequence 226, App
2	840	41.3	351	US-09-978-697-226	Sequence 226, App
3	840	41.3	351	US-09-978-192A-226	Sequence 226, App
4	840	41.3	351	US-09-999-832A-226	Sequence 226, App
5	840	41.3	351	US-09-978-189-226	Sequence 226, App
6	840	41.3	351	US-10-174-590-80	Sequence 80, App
7	840	41.3	351	US-10-176-758-80	Sequence 80, App
8	840	41.3	351	US-10-175-737-80	Sequence 80, App
9	840	41.3	351	US-10-173-706-80	Sequence 80, App
10	840	41.3	351	US-10-175-738-80	Sequence 80, App
11	840	41.3	351	US-10-175-752-80	Sequence 80, App
12	840	41.3	351	US-10-176-482-80	Sequence 80, App
13	840	41.3	351	US-10-176-757-80	Sequence 80, App
14	840	41.3	351	US-10-176-913-80	Sequence 80, App
15	840	41.3	351	US-10-180-552-80	Sequence 80, App
16	840	41.3	351	US-10-180-557-80	Sequence 80, App
17	840	41.3	351	US-10-173-700-80	Sequence 80, App
18	840	41.3	351	US-10-174-572-80	Sequence 80, App
19	840	41.3	351	US-10-174-579-80	Sequence 80, App

20	840	41.3	351	US-10-174-582-80	Sequence 80, App
21	840	41.3	351	US-10-174-586-80	Sequence 80, App
22	840	41.3	351	US-10-175-739-80	Sequence 80, App
23	840	41.3	351	US-10-175-740-80	Sequence 80, App
24	840	41.3	351	US-10-175-743-80	Sequence 80, App
25	840	41.3	351	US-10-176-489-80	Sequence 80, App
26	840	41.3	351	US-10-176-492-80	Sequence 80, App
27	840	41.3	351	US-10-176-747-80	Sequence 80, App
28	840	41.3	351	US-10-176-750-80	Sequence 80, App
29	840	41.3	351	US-10-176-985-80	Sequence 80, App
30	840	41.3	351	US-10-176-987-80	Sequence 80, App
31	840	41.3	351	US-10-176-991-80	Sequence 80, App
32	840	41.3	351	US-10-176-992-80	Sequence 80, App
33	840	41.3	351	US-10-176-993-80	Sequence 80, App
34	840	41.3	351	US-10-184-658-80	Sequence 80, App
35	840	41.3	351	US-10-173-695-80	Sequence 80, App
36	840	41.3	351	US-10-173-697-80	Sequence 80, App
37	840	41.3	351	US-10-173-705-80	Sequence 80, App
38	840	41.3	351	US-10-174-576-80	Sequence 80, App
39	840	41.3	351	US-10-174-585-80	Sequence 80, App
40	840	41.3	351	US-10-174-586-80	Sequence 80, App
41	840	41.3	351	US-10-176-481-80	Sequence 80, App
42	840	41.3	351	US-10-176-485-80	Sequence 80, App
43	840	41.3	351	US-10-176-487-80	Sequence 80, App
44	840	41.3	351	US-10-176-493-80	Sequence 80, App
45	840	41.3	351	US-10-176-493-80	Sequence 80, App

ALIGNMENTS

RESULT 1  
US-09-978-295A-226  
Sequence 226, Application US/09/978-295A  
Parent No. US200156106A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Bostoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Ford, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Jeddard, Audrey  
APPLICANT: Jedowski, Paul J.  
APPLICANT: Krimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Klayman, Ivan J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoletti, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Janie  
APPLICANT: Williams, F. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978-295A  
CURRENT FILING DATE: 2001-10-15  
PRIORITY APPLICATION NUMBER: 09/714585  
PRIORITY FILING DATE: 2001-07-30  
PRIORITY APPLICATION NUMBER: 60/062250  
PRIORITY FILING DATE: 1997-10-17  
PRIORITY APPLICATION NUMBER: 60/064249

[illegible]

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? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085700
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085689
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085579
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085580
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085573
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085704
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085697

Query Match          41.3% Score 840; DB 9; Length 351;
Best Local Similarity 44.8%; Pred. No. 1,1e-69;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

QY 14 TLLALALPAALANSSGRMMGIVNASTNLDSKSLQVLPSLQLSRKGRRLIR 73
DB 9 SCLRLVAFVSAASH-----WLYLAKLSVGSISEETICE-----KLGLLQKQVQM* 58
QY 74 QNPGLHSVSGLSQAVRECKWQFRNRNMWCTAPAPHLFGKIVNRGCEIATFIAITSA 133
DB 59 RNLEVMDSYRGKQALIECCOYQFRNRNMWCTILDLPVFGKIVTQGTREAFVYAISSA 118
QY 134 GVTSHVARGSGESISTECTCDYRRRGPGGPDMMWGSGSDNIDFGRLFGRGEFVDSGKGR- 192
DB 119 GVAFAVTRACSSSELEKCGCDRTYHVSPOGFOMSGSDNIAIVAFSGSPVDYVERKRG 178
QY 193 -DLRFLMNLHNEAGRTTVESEKROCKCHNGSSCTVKTQWRLFTLRANGDYLRDRF 250
DB 179 ASSRALMLNLHNEAGRKALITHRVCKRGHSGSCVKTQWRAVPPFQVGHALKRKF 238
QY 251 DGASRVLYGNGRGNRSPRAELLREPEDPAHRKPPSPHDLVYFEKSPNFCYSGRLGTAGT 310
DB 239 DGATEVEPRPVSSRA-----LVPNAGFKPHIDEDLVYLERSPFCQDMRGJVT 291
QY 311 AGRCANSSPALDGCCLCCGGRGRTQVTERNCNCFHHCIVSRNCTHRTVLRHNC 369
DB 292 RGTCNKTSKAIDGCLCCGRGRTQVTERNCNCFHHCIVSRNCTHRTVLRHNC 350

RESULT 2
Sequence 226, Application US/09978697
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi
? APPLICANT: Baker Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dan
? APPLICANT: Ferrara, Napoleon
? APPLICANT: Filzvaroff, Ellen
? APPLICANT: Fonq, Sherman
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Garber, Hanspeter
? APPLICANT: Gerlitsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austen L.
? APPLICANT: Hillan, Kenneth J
? APPLICANT: Kiljavin, Ivar J.
? APPLICANT: Kuo, Sophia S.
? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James.
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Shelton, David L.
? APPLICANT: Stewart, Timothy A.

APPLICANT: Tomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William L.
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585.
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/061249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/080227
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PRIOR APPLICATION NUMBER: 60/080248
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081870
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? PRIOR FILING DATE: 1998-04-08
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? PRIOR APPLICATION NUMBER: 60/085573
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085764
? PRIOR FILING DATE: 1998-05-15
? PRIOR APPLICATION NUMBER: 60/085697

Query Match      41.3%  Score 8401  DB 9: 160416.351
Best Local Similarity 44.8%  Pred. No. 12e-69;
Matches 161:  Conservative  5%:  Mismatches 123:  100%  20:  34%  4:

QY  14 TLLALALALALAAANSSRRMGIVYANVASTNLLTSSKGLVLEFPRCLSKKQKHLIR  73
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1b  3 SELLVFAVNSAASN-----WLTAKLSVSGSISEETCE-----KIKLIDKQWCKR  58
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  74 QNGLIHNSNGLSGAVNFECKWQFNRKMNPTAPRPLFGRIVNHPDEFAIFATISA  133
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2b  59 RILEVDSVFHGAULALEEYOFPNRMNSTLIDLPFGKVVTLQTHPAFVAYMISA  118
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  134 GYHSVARSSESSIESCTGDRHRRGPGQDWHWGSCNIIHFCLEHPEVYNSCKGR-  192
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1a  119 GAFAVTAACSGTELEKSTDRTVGVSPGFQWSCSDNIAYVAAAS-SPVYPRRSKG  178
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  193 -DLRFNLNHNNAIGTIVSEHREQCKCHGMSGGCTVETGMPLLILAAVDVLEHFF  250
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2b  179 ASSSRALNHNNAIGRAKAILTHMRVECKCHGVSGCEVKTQMAVFFPHVGHALKRFF  238
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  251 DGSATVLYGNPSSRSPASFAELLRLREDPAPKPPSPHDLVYPERKSPNATYSGHITAT  310
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1b  239 DGRTEVERHVGSSRA-----LVPRNAQFKRHTEDELVLIELSPHFLEDMHSVALST  291
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  311 AGACNSSPALDGCCLCGCGHRTFRTORYTERCNCSTRHCKCHVSRNCTIIRVULHEC  369
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1b  292 RRTGNKTSKAIIDCCELLCGCGFHITAQVLAERKSCKTRHMCQCFKCPJOKLVELHTC  350
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RESULT 3
US-09-978-192A-226
Sequence 226, Application US/09978192A
Patent No. US200207755381
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnogyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filyaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gettel, Hanspeter
APPLICANT: Gettisen, Maty E.

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APPLICANT :	Godowski, Paul J.	PRIOR APPLICATION NUMBER :	60/080105
APPLICANT :	Gimaldi, J Christopher	PRIOR FILING DATE :	1998-03-31
APPLICANT :	Guirey, Austin L.	PRIOR APPLICATION NUMBER :	60/080194
APPLICANT :	Hillan, Kenneth J.	PRIOR FILING DATE :	1998-03-31
APPLICANT :	Kiljavin, Ivar J.	PRIOR APPLICATION NUMBER :	60/080327
APPLICANT :	Kuo, Sophia S.	PRIOR FILING DATE :	1998-04-03
APPLICANT :	Napier, Mary A.	PRIOR APPLICATION NUMBER :	60/080328
APPLICANT :	Paoli, Nicholas F.	PRIOR FILING DATE :	1998-04-03
APPLICANT :	Roy, Margaret Ann	PRIOR APPLICATION NUMBER :	66/080333
APPLICANT :	Shelton, David L.	PRIOR FILING DATE :	1998-04-01
APPLICANT :	Stewart, Timothy A.	PRIOR APPLICATION NUMBER :	40/080334
APPLICANT :	Thomas, Daniel	PRIOR FILING DATE :	1998-04-06
APPLICANT :	Williams, P. Mickey	PRIOR APPLICATION NUMBER :	60/080407
APPLICANT :	Wood, William L.	PRIOR FILING DATE :	1998-04-05
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic			
FILE REFERENCE: P2530109			
CURRENT APPLICATION NUMBER: US/09/378,192A			
PRIOR FILING DATE :	2001-10-15	PRIOR APPLICATION NUMBER :	09/918585
PRIOR FILING DATE :	2001-07-30	PRIOR APPLICATION NUMBER :	60/062250
PRIOR FILING DATE :	1997-10-17	PRIOR APPLICATION NUMBER :	60/064249
PRIOR FILING DATE :	1997-11-03	PRIOR APPLICATION NUMBER :	60/065311
PRIOR FILING DATE :	1997-11-13	PRIOR APPLICATION NUMBER :	60/066364
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PRIOR FILING DATE :	1998-03-13	PRIOR APPLICATION NUMBER :	60/078004
PRIOR FILING DATE :	1998-03-20	PRIOR APPLICATION NUMBER :	60/078886
PRIOR FILING DATE :	1998-03-20	PRIOR APPLICATION NUMBER :	60/078936
PRIOR FILING DATE :	1998-03-20	PRIOR APPLICATION NUMBER :	60/078910
PRIOR FILING DATE :	1998-03-20	PRIOR APPLICATION NUMBER :	60/078939
PRIOR FILING DATE :	1998-03-20	PRIOR APPLICATION NUMBER :	60/079294
PRIOR FILING DATE :	1998-03-25	PRIOR APPLICATION NUMBER :	60/079656
PRIOR FILING DATE :	1998-03-26	PRIOR APPLICATION NUMBER :	60/079664
PRIOR FILING DATE :	1998-03-27	PRIOR APPLICATION NUMBER :	60/079689
PRIOR FILING DATE :	1998-03-27	PRIOR APPLICATION NUMBER :	60/079653
PRIOR FILING DATE :	1998-03-27	PRIOR APPLICATION NUMBER :	60/079728
PRIOR FILING DATE :	1998-03-27	PRIOR APPLICATION NUMBER :	60/079786
PRIOR FILING DATE :	1998-03-27	PRIOR APPLICATION NUMBER :	60/079920
PRIOR FILING DATE :	1998-03-30	PRIOR APPLICATION NUMBER :	60/079923
PRIOR FILING DATE :	1998-03-30	PRIOR APPLICATION NUMBER :	60/080105
PRIOR FILING DATE :	1998-03-31	PRIOR APPLICATION NUMBER :	60/080107
PRIOR FILING DATE :	1998-03-31	PRIOR APPLICATION NUMBER :	60/080107

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Query Match      41.3%; Score 640; 28 5; Length 351;
Best Local Similarity 44.6%; Pred. No. 1,1-69;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4

QY      14 TLTLALALPALAANSSGRMKQIVVAVSSNLLTKSKYQLVEPSTQLLSKQKELTP 73
Db       9 SLTLVAVFVAASNN-----WYLAKLSVGSSEHECTE-----KKSLIRQVQMK 59
QY      74 QNPILSHVSGQLQVAHECKQWQFNFRMNPTAPGHLGKIVNKGQRETAIFAITS 133
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QY      134 GYTSVAVRVSSEGSJFHSCTCDYKRRKPGFPMHMYLNINIDFGLRREFVNSDKR 192
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QY      193 --DLRFLMLDHNNGRRTTYSEMRQEKQMGMSGYTATQWMLPTLAAVDYLRQF 250
Db     179 ASSSRALMLDHNNGRKRLLTHRVECKQGVSGSEVKTQWRAVPFRQVGHAKRF 238
QY      251 DGASRVLYGRRGSSNASHALLLEFEDPAKRPSPRDLVEYKSPNFCYTSRGLTAT 310
Db     238 DGATEVEPRRVSSA-----LVRRNAQKRPHTDEVLVEPSPFCQDMRSVGLGT 291
QY      311 AGRACNSSPALDQJCELCGGRGRTPTQPTENCTFRHMCVSCNNTHTRVLHET 369
Db     292 RGRRCNKSTKALDQJCELCGGRGFHTAQLAEKGSKRHWCCPFKMGQGRNLVELHTC 350

RESULT 4
US-09-999-812A-226
Sequence 226, Affiliation 95/999/9812A

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Patent No. 3,820,927

GENERAL INFORMATION

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Borstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Ford, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gether, Hans-Peter

APPLICANT: Getritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kiljavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Kapler, Mary A.

APPLICANT: Pau, James.

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tomas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P26301C63

CURRENT APPLICATION NUMBER: US/09/399,832A

CURRENT FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-11

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

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PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079663



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Gy 251 DGASHVLYGNKSNRASHRAEALLRLLEPCBAKHPSHULVFEKSNCECTSYSLGIAT: 310
Db 239 DGAIEVERRRVGGSSRA-----LVPRNAOKRPHTIDDLVYLEPSPDCEOMRSTYLSI 291
Gy 311 AGACNSSSPALDGCCLCCGCGHRTFORVTEFCNCTIHWCCCHVSCNCTHTFVLHCO 369
Db 292 RGRITNKTSKAIIDCCCLCCGCGHRTAQVLAERCS:KTHWCCFKVRCOCORLVEIHTC 350

RESULT 5
US-09-978-189-226
; Sequence 226, Application US/09978189
; Publication No. US2003004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Kito, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William L.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P107
; CURRENT APPLICATION NUMBER: US/09/978,189
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/718585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079785
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081043
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
```

Page 9

```
QY      14 TLLALLAALPAALANSSGRMWGIVNASSTNLTDKSLÖVLEPSLÖLSRKÖRLIR 73
        :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
```

```

RESULT: 6
US-10-174-590-80
Sequence 80, Application US/10174590
Publication No. US20031008352A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chin, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Joddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colib K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenli
TITLE OF INVENTION: SECRETED ANT. TRANSMEMBRANE P. ACTIVITIES AND NUCLEOT.
TITLE OF INVENTION: AIDS ENCODING THE SAME
FILE REFERENCE: P4330R042
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior application removed. See file wrapper of part
NUMBER OF SEQ. ID NOS: 612
SEQ. ID NO. 80
LENGTH: 351
TYPE: prt
ORGANISM: Homo Sapien
US-10-174-590-80

```

```

Query Local Similarity 44.3% Score 840 DB: Length 351:
Best Local Similarity 44.8% Pred. No. 116-6%
Matches 161: Conservative 55: Mismatches 124: Gaps 26: Caps

QY 14 TLILAALPALAANSGGMMGIVNASSINLTDSKSLVLEFSLQLSKRQFFLR 73
DB 9 SLRLVFAVEAASN----NLYLAKLSVGSISEETD-----KLGIDPQVMKR 58
QY 74 QNGGILHSVSLDSAVRECKQCFNRNRMNPTAPGHELEFLVNNPRTAFIPATSA 13
DB 59 RLEKWSIVRPGDGLALEECQVDFPNRRMNSTLSDLPFGQVNYGYTREAAYVATSA 11
QY 134 GYTHVASVNGSEDSINSCTDIFRPGPGGPPMHMGSCNITVGVNIGREFVDSGKR- 19
DB 119 GAAEAVTPAGSSSELEKQGGTRFVHVSQPGFQSGSGSNIAVIVASQSVLEFSSKG 178
QY 193 -ELPLNUNNNAJPTYESMGECKSGSGSTAYTNGGFLPRLAVSLVIRKE 255
DB 179 ASSPRLMNNNNACKALKLLHMPVERKQVSGSGSLVKIWKAVNPFQVYHAKREF 235
QY 231 GAAVYVGNNGSRKASHALLLEEFEDPAIRPSPADLVTEFKSPNCTVSGHGAII 51

```

```

Db      239 DGAIEVFRFVSSRA-----LVRRNQRPHIDEDLVLEPSPDFEQLMR-
      311 AGRACSSSPALDGCCELLCGRGHRTORTVTERNCNCTFFHWCCHVSCRNCHTIVLEEC
      292 KGRCKKTSKALDGCCELLCGRGHRTAQVELAERCSKCFHWCCEVFCQCGQCVLVELHTC

```

## RESULT 7

US-10-176-758-80

```

? Sequence 80, Application US/10176758
? Publication No. US2003008353A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Chen, Jian
? APPLICANT: Desnoyers, Luc
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Pan, James
? APPLICANT: Smith, Victoria
? APPLICANT: Malanabe, Colin K.
? APPLICANT: Wood, William L.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NOCLEIC
? FILE REFERENCE: P430R1C104
? CURRENT APPLICATION NUMBER: US/10/176,758
? PRIOR APPLICATION REMOVED - See File Wrapper of Palm
? NUMBER OF SEQ ID NOS: 612
? SEQ ID NO 80
? LENGTH: 351
? TYPE: PRT
? ORGANISM: Homo Sapien
US-10-176-758-80

```

```

Query Match      41.3% Score 840: DB 9: Length 351:
Best Local Similarity 44.8% Pred. No. 1,1e-69:
Matches 161: Conservative 55: Mismatches 123: Indels 20: Gaps 4:

```

```

QY      14 TLLALALFALANSSSRKMGIVVAVASTNLTIDSKSLQVLPEPSDLSKQRLIR 73
      9 SRLILFAVFAASAASN-----WLYLAKLSVSGSISEEICE-----KLGGLIQGVQWCK 58
      74 QNPGILHSVSGLSAVRECKWQFRNRWNCPTAPGHLEFGKLVNCGRETAIFATISA 133
      59 RNEVMDSVRGQALALEECYQYOFNRNRWNCSTLDSLPFGKVVTOGTREAFVYATISA 118
      134 GVTHSVANSGSGSIESCTGDIYRRGPGSPDMHWGCSNDIFGHLFGRHLYVDSGEGR- 192
      119 GVAFAVTRACSGGELEKCGDRTVHGVSPOGQWSSGSDNIAYGVAFSOSFVIVRERSKG 178
      193 --DLRFIMLNHNNGRITVSEMPQECKCHMSGCTVTCMPLPTLRAVGVLEDRF 250
      179 ASSSRALNHNNGRITVSEMPQECKCHMSGCTVTCMPLPTLRAVGVLEDRF 238
      251 DGASRYLYNKGSRASRAELLEDEPAPKPPSHULVYFKSNFPTTSGVLACT 310
      239 DGAIEVFRFVSSRA-----LVRRNQRPHIDEDLVLEPSPDFEQLMR 292
      311 AGRACSSSPALDGCCELLCGRGHRTAQVELAERCSKCFHWCCEVFCQCGQCVLVELHTC 350
      292 KGRCKKTSKALDGCCELLCGRGHRTAQVELAERCSKCFHWCCEVFCQCGQCVLVELHTC 350

```

## RESULT 8

US-10-175-737-80

```

? Sequence 80, Application US/10175737
? Publication No. US2003001315A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Chen, Jian

```

```

? APPLICANT: Desnoyers, Luc
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Pan, James
? APPLICANT: Smith, Victoria
? APPLICANT: Malanabe, Colin K.
? APPLICANT: Wood, William L.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NOCLEIC
? FILE REFERENCE: P430R1C104
? CURRENT APPLICATION NUMBER: US/10/175,737
? PRIOR APPLICATION REMOVED - See File Wrapper of Palm
? NUMBER OF SEQ ID NOS: 612
? SEQ ID NO 80
? LENGTH: 351
? TYPE: PRT
? ORGANISM: Homo Sapien
US-10-175-737-80

```

```

Query Match      41.3% Score 840: DB 9: Length 351:
Best Local Similarity 44.8% Pred. No. 1,1e-69:
Matches 161: Conservative 55: Mismatches 123: Indels 20: Gaps 4:

```

```

QY      14 TLLALALFALANSSSRKMGIVVAVASTNLTIDSKSLQVLPEPSDLSKQRLIR 73
      9 SRLILFAVFAASAASN-----WLYLAKLSVSGSISEEICE-----KLGGLIQGVQWCK 58
      74 QNPGILHSVSGLSAVRECKWQFRNRWNCPTAPGHLEFGKLVNCGRETAIFATISA 133
      59 RNEVMDSVRGQALALEECYQYOFNRNRWNCSTLDSLPFGKVVTOGTREAFVYATISA 118
      134 GVTHSVANSGSGSIESCTGDIYRRGPGSPDMHWGCSNDIFGHLFGRHLYVDSGEGR- 192
      119 GVAFAVTRACSGGELEKCGDRTVHGVSPOGQWSSGSDNIAYGVAFSOSFVIVRERSKG 178
      193 --DLRFIMLNHNNGRITVSEMPQECKCHMSGCTVTCMPLPTLRAVGVLEDRF 250
      179 ASSSRALNHNNGRITVSEMPQECKCHMSGCTVTCMPLPTLRAVGVLEDRF 238
      251 DGASRYLYNKGSRASRAELLEDEPAPKPPSHULVYFKSNFPTTSGVLACT 310
      239 DGAIEVFRFVSSRA-----LVRRNQRPHIDEDLVLEPSPDFEQLMR 292
      311 AGRACSSSPALDGCCELLCGRGHRTAQVELAERCSKCFHWCCEVFCQCGQCVLVELHTC 350
      292 KGRCKKTSKALDGCCELLCGRGHRTAQVELAERCSKCFHWCCEVFCQCGQCVLVELHTC 350

```

## RESULT 9

US-10-173-706-80

```

? Sequence 80, Application US/10173706
? Publication No. US2003002203A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Chen, Jian
? APPLICANT: Desnoyers, Luc
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Pan, James
? APPLICANT: Smith, Victoria
? APPLICANT: Malanabe, Colin K.
? APPLICANT: Wood, William L.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NOCLEIC
? FILE REFERENCE: P430R1C107
? CURRENT APPLICATION NUMBER: US/10/173,706
? PRIOR APPLICATION REMOVED - See File Wrapper of Palm

```





RESULT 13  
US-10-176-757-80  
; Sequence 80, Application US/101767575  
; Publication No. US200330022297A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Deshpande, Iraj  
; APPLICANT: Goddard, Audrey

```

1  APPLICANT: Zhang Zhenli
2  TITLE OF INVENTION: SEQUESTED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIDE
3  TITLE OF INVENTION: ACIDS ENCODING THE SAME
4  FILE REFERENCE: P430R1066
5  CURRENT APPLICATION NUMBER: US/07/76,913
6  CURRENT FILING DATE: 2002-06-20
7  Prior Application removed - See file Wrapper of Palm
8  NUMBER OF SEQ ID NOS: 612
9  SEQ ID NO: 80

```



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: April 22, 2003, 16:37:37 : Search time 46 Seconds

(without alignments)  
771,295 Million cell updates/sec

Title: US-09-674-292-1

Perfect score: 2036

Sequence: 1 MSIMALLPGWVSATLLALAL.....WCHVSCRNCTHTPVLEHC 370

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-73:\*  
1: PIR:\*  
2: PIR:\*  
3: PIR:\*  
4: PIR:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2036	100.0	370	1	TVHUT1 transforming prote
2	2021	99.3	370	1	TVHUT1 transforming prote
3	2021	99.3	370	1	TVHUT1 transforming prote
4	1671	82.1	369	2	S18721 Mnt-1 protein prec
5	1595	78.3	370	2	S15013 Mnt-1 protein - ze
6	1463	71.9	371	1	TVXLT1 transforming prote
7	1022.5	50.2	468	1	A29650 wingless (wg) prot
8	998	49.0	469	1	TVFPT1 transforming prote
9	873.5	42.9	352	2	A49146 developmental regu
10	866.5	42.5	303	2	S41155 wingless protein -
11	843.5	41.4	352	2	A35503 Mnt-3A protein - m
12	843.5	41.4	355	2	A35503 Mnt-3A protein - m
13	836	41.1	351	2	C36470 Mnt-4 protein - mo
14	827	40.6	351	2	JC2451 Mnt-4 protein pre
15	822.5	40.4	352	2	A48828 wingless homolog X
16	787.5	38.7	365	2	JC7694 soluble-type glyco
17	785	38.6	360	2	S00834 Mnt-1-like protein
18	781	38.4	360	2	B36470 Mnt-2 protein - mo
19	780.5	38.3	364	2	F36470 Mnt-2 protein - mo
20	769	37.8	379	2	D36470 Mnt-5A protein - m
21	766.5	37.6	365	2	A48828 Mnt-4 protein - mo
22	766.5	37.6	372	2	T09612 secreted glycoprot
23	759.5	37.3	333	2	A47535 gene WNT3 protein
24	753	37.0	359	2	A56549 cell-cell signalin
25	749	36.8	372	2	B36470 Mnt-5b protein - m
26	742	36.4	417	2	B59392 Mnt10a protein pro
27	741	36.4	417	2	JC7693 soluble-type glyco
28	728.5	35.8	357	2	B56549 cell-cell signalin
29	724.5	35.6	360	2	S34173 Mnt-5c protein - A

30	722.5	35.5	442	2	150110 Mnt10a protein - z
31	716.5	35.2	449	2	B36470 Mnt-7b protein - m
32	711.5	34.9	449	2	144770 Mnt-7a protein - m
33	707	34.7	369	2	149463 potential oncogene
34	707	34.7	369	2	A59492 Mnt10b protein pre
35	702	34.5	360	2	126037 hypofunctional prote
36	694	34.1	360	2	84495 Mnt-2 protein
37	696	33.9	334	2	150729 gene Mnt-1 protein
38	684	33.6	352	2	S24559 Mnt-2 protein - fr
39	678	33.3	348	2	110502 Mnt-7a protein - fr
40	671	33.0	1004	2	A48821 Mnt-5 protein - fr
41	660.5	32.4	354	2	S34378 Mnt-11 protein - m
42	641	31.5	353	2	151572 maternal protein - Ca
43	631	31.0	372	2	S34694 Mnt-1 protein - Ca
44	630.5	31.0	354	2	JC4152 Mnt-11 protein pre
45	630.5	31.0	359	2	150505 gene mnt10 protein

## ALIGNMENTS

## RESULT 1

TVHUT1 transforming protein [nt-1] - human

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1997 #Sequence-Revision 30-Sep-1997 #\* \* \* Change 16-Jun-1999

C:Accession: A24674

R:van Ooyen, A.; Kwee, V.; Nusse, R.

EMBL J. 4, 29,5-299, 1985

A:Title: The nucleotide sequence of the human int-1 homology oncogene: evolutionary

A:Reference number: A24674; MIM:6055728; PMID:2944712

A:Accession: A24674

A:Molecule type: DNA

A:Residues: 1-370 &lt;VAN&gt;

A:Cross-References: GB:X03072; NID:933935; PIDN:CA24674.1; PID:933936

C:Genetics:

A:Gene: GDB:WNT1; INT1

A:Cross-References: GDB:120101; OMIM:164820

A:Map position: 12q13-12q14

A:Introns: 35/2; 120/1; 208/3

C:Superfamily: Mnt-1 transforming protein

C:Keywords: proto-oncogene; transforming protein; transmembrane protein

F1:48/Domain: transmembrane \*status predicted &lt;TM&gt;

Query Match	100.0%	Score 2036	DB 1	Length 370
Best Local Similarity	100.0%	Pred. No. 1.8e-158		
Matches 370	Conservative	0	Mismatches 0	Indels 0
			Gaps 0	
QY	1	MSIMALLPGWVSATLLALALFAALANSSGRWGIWVASTNLDKSTQTLVLEPS	60	
DB	1	MLHWALIFWVSATLLALALFAALANSSGRWGIWVASTNLDKSTQTLVLEPS	60	
QY	61	LOLLSKKRLRQNGGILHSV3LQSAVRECKQFRKKHND1MAQGHLECKLVNNG	120	
DB	61	LOLLSKKRLRQNGGILHSV3LQSAVRECKQFRKKHND1MAQGHLECKLVNNG	120	
QY	121	CHETFAIPLAISAGVTHSVARSQSGSIESGTCDDYRRRQSG3FWMHMGSCSDNIDGRFL	180	
DB	121	CHETFAIPLAISAGVTHSVARSQSGSIESGTCDDYRRRQSG3FWMHMGSCSDNIDGRFL	180	
QY	181	GHEFTNSSEKRDLEFLMN1HNREGRTVSEKRECK3HNS3STVTCMRLPTLR	240	
DB	181	GHEFTNSSEKRDLEFLMN1HNREGRTVSEKRECK3HNS3STVTCMRLPTLR	240	
QY	241	AVGVTLPRFGASPVLYNCRQSNFASAEILLLEPDAFAK71SHDLVFEKSNFCT	300	
DB	241	AVGVTLPRFGASPVLYNCRQSNFASAEILLLEPDAFAK71SHDLVFEKSNFCT	300	
QY	301	VSGLRTGTAGTARCNSSSPALDSCGLCCGGRHRTKRTVTH1N1TFMCRHVSCHNC	360	
DB	301	VSGLRTGTAGTARCNSSSPALDSCGLCCGGRHRTKRTVTH1N1TFMCRHVSCHNC	360	
QY	361	THHPVLEHC 370		

Db 361 THTRVLHECL 370

# RESULT 2

TRANS1

Transforming protein int-1 - mouse

N:Alternate names: int-1 protein

C:Species: Mus musculus (house mouse)

C:Date: 17-Mar-1987 \*sequence\_revision 17-Mar-1987 \*text\_change 18-Jun-1999

C:Accession: A23447; A36470; A01358

R:Func: Y.K.T.: Shackelford, G.M.; Brown, A.M.; Sanders, G.S.; Varms, H.E.

Mol. Cell. Biol. 5, 3337-3344, 1985

A:Title: Nucleotide sequence and expression in vitro of cDNA derived from mRNA of int-1.

A:Reference number: A9368; M01D:8510810; PMID:373829

A:Accession: A23447

A:Molecule type: mRNA

A:Residues: 1-370 <F0N>

A:Cross-references: GB:M1943; NID:q198423; PIRN:AAA9322.1; PID:q293671

A>Note: the authors translated the codon GTG for residue 242 as Gly and GGC for codon 24

R:Gavin, B.J.; McMahon, J.A.; McMahon, A.P.

Genes Dev. 4, 2319-2332, 1990

Title: Expression of multiple novel int-1/int-1-related genes during fetal and adult m

Reference number: A36470; M01D:91122634; PMID:2279700

A:Accession: A36470

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-370 <GAV>

C:Genetics:

A:Gene: int-1

A:Introns: 35/2; 126/1; 208/3

C:Superfamily: int-1 transforming protein

C:Keywords: proto-oncogene; transforming protein; transmembrane protein

F1-48/Domain: transmembrane \*status predicted <TM>

Query Match 99.3%; Score 2021; DB 1; Length 370;

Best Local Similarity 98.9%; Pred. No. 3.1e-159;

Matches 366; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 1 MGIMALLPQWVSATLLALALPALAANSSGRWGWIVNASTNTLTSKSLQVLEPS 60

Db 1 MGIMALLPQWVSATLLALALPALAANSSGRWGWIVNASTNTLTSKSLQVLEPS 60

Qy 61 LQLSKRQKRLIRQNPGLHSVSGLSAVRECKWQFRRNPNCTAAPHLEFKIVNKG 120

Db 61 LQLSKRQKRLIRQNPGLHSVSGLSAVRECKWQFRRNPNCTAAPHLEFKIVNKG 120

Qy 121 CRETAIFAITSAGVTSVAKSCSESSICSTCDYRRKGPGGPDHMGSCSNTIDPGRLE 180

Db 121 CRETAIFAITSAGVTSVAKSCSESSICSTCDYRRKGPGGPDHMGSCSNTIDPGRLE 180

Qy 121 GREFVDSGKGRDLRFPLNHNNEAGRTVSEMKQCKCHGNSGSCIVPTCKMLPTLR 240

Db 181 GREFVDSGKGRDLRFPLNHNNEAGRTVSEMKQCKCHGNSGSCIVPTCKMLPTLR 240

Qy 241 AVGVLRDFPDGASRVLYGNKSNRASRAELRLREPEPAHRRPSPHDVYFEKSPNCT 300

Db 241 AVGVLRDFPDGASRVLYGNKSNRASRAELRLREPEPAHRRPSPHDVYFEKSPNCT 300

Qy 301 YSGRLTATAGACRACNSSPALLDGCCLCCGGRHRTQVTERNCNFFRCHVSCRNC 360

Db 301 YSGRLTATAGACRACNSSPALLDGCCLCCGGRHRTQVTERNCNFFRCHVSCRNC 360

Qy 361 THTRVLHECL 370

Db 361 THTRVLHECL 370

# RESULT 3

TRANS1

Transforming protein int-1 - mouse mammary tumor virus

C:Species: mouse mammary tumor virus, MMTV

C:Date: 31-Dec-1991 \*sequence\_revision 31-Dec-1991 \*text\_change 18-Jun-1999

TRANS1

Transforming protein int-1 - mouse mammary tumor virus

C:Species: mouse mammary tumor virus, MMTV

C:Date: 31-Dec-1991 \*sequence\_revision 31-Dec-1991 \*text\_change 18-Jun-1999

TRANS1

Transforming protein int-1 - mouse mammary tumor virus

C:Species: mouse mammary tumor virus, MMTV

C:Date: 31-Dec-1991 \*sequence\_revision 31-Dec-1991 \*text\_change 18-Jun-1999

TRANS1

Transforming protein int-1 - mouse mammary tumor virus

C:Species: mouse mammary tumor virus, MMTV

C:Date: 31-Dec-1991 \*sequence\_revision 31-Dec-1991 \*text\_change 18-Jun-1999

TRANS1

Transforming protein int-1 - mouse mammary tumor virus

C:Species: mouse mammary tumor virus, MMTV

C:Date: 31-Dec-1991 \*sequence\_revision 31-Dec-1991 \*text\_change 18-Jun-1999

TRANS1

Transforming protein int-1 - mouse mammary tumor virus

C:Species: mouse mammary tumor virus, MMTV

C:Date: 31-Dec-1991 \*sequence\_revision 31-Dec-1991 \*text\_change 18-Jun-1999

TRANS1

Transforming protein int-1 - mouse mammary tumor virus

C:Species: mouse mammary tumor virus, MMTV

C:Date: 31-Dec-1991 \*sequence\_revision 31-Dec-1991 \*text\_change 18-Jun-1999

C:Accession: B23447; A01358; A23447

R:Ogden, A.V.; Nusse, R.

Cell 79, 231-247, 1994

A:Title: Structure and nucleotide sequence of the putative mammary oncogene int-1; pr

A:Reference number: A90855; M01D:85024897; PMID:6091914

A:Accession: B23447

A:Molecule type: cDNA

A:Residues: 1-370 <DOY>

A:Cross-references: EMBL:K02533; NID:q198423; PIRN:AAA9322.1; PID:q293671

A>Note: the authors translated the codon GTG for residue 242 as Gly and GGC for codon

C:Genetics:

A:Gene: int-1

A:Introns: 35/2; 126/1; 208/3

C:Superfamily: int-1 transforming protein

C:Keywords: oncogene; transforming protein; transmembrane protein

F10-25/Domain: transmembrane \*status predicted <TM>

Query Match 99.3%; Score 2021; DB 1; Length 370;

Best Local Similarity 98.9%; Pred. No. 3.1e-159;

Matches 366; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 1 MGIMALLPQWVSATLLALALPALAANSSGRWGWIVNASTNTLTSKSLQVLEPS 60

Db 1 MGIMALLPQWVSATLLALALPALAANSSGRWGWIVNASTNTLTSKSLQVLEPS 60

Qy 61 LQLSKRQKRLIRQNPGLHSVSGLSAVRECKWQFRRNPNCTAAPHLEFKIVNKG 120

Db 61 LQLSKRQKRLIRQNPGLHSVSGLSAVRECKWQFRRNPNCTAAPHLEFKIVNKG 120

Qy 121 CRETAIFAITSAGVTSVAKSCSESSICSTCDYRRKGPGGPDHMGSCSNTIDPGRLE 180

Db 121 CRETAIFAITSAGVTSVAKSCSESSICSTCDYRRKGPGGPDHMGSCSNTIDPGRLE 180

Qy 121 GREFVDSGKGRDLRFPLNHNNEAGRTVSEMKQCKCHGNSGSCIVPTCKMLPTLR 240

Db 181 GREFVDSGKGRDLRFPLNHNNEAGRTVSEMKQCKCHGNSGSCIVPTCKMLPTLR 240

Qy 241 AVGVLRDFPDGASRVLYGNKSNRASRAELRLREPEPAHRRPSPHDVYFEKSPNCT 300

Db 241 AVGVLRDFPDGASRVLYGNKSNRASRAELRLREPEPAHRRPSPHDVYFEKSPNCT 300

Qy 301 YSGRLTATAGACRACNSSPALLDGCCLCCGGRHRTQVTERNCNFFRCHVSCRNC 360

Db 301 YSGRLTATAGACRACNSSPALLDGCCLCCGGRHRTQVTERNCNFFRCHVSCRNC 360

Qy 361 THTRVLHECL 370

Db 361 THTRVLHECL 370

# RESULT 4

TRANS1

int-1 protein precursor, secreted - axolotl

C:Species: Ambystoma mexicanum (axolotl)

C:Date: 21-Nov-1993 \*sequence\_revision 10-Nov-1995 \*text\_change 16-Jun-1999

C:Accession: S13721; S13722

R:Busse, U.; Guay, J.; Seguin, C.

Nucleic Acids Res. 19, 981-1991

A:Title: Nucleotide sequence of a cDNA encoding int-1 of the Mexican axolotl

A:Reference number: S13721; M01D:91081334; PMID:2259633

A:Accession: S13721

A:Molecule type: mRNA

A:Residues: 1-369 <BUS>

A:Cross-references: EMBL:X55270; NID:q62424; PIRN:CAA9370.1; PID:q2425

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993

C:Genetics:

A:Gene: int-1

C:Superfamily: int-1 transforming protein

Query Match 82.1%; Score 1671; DB 2; Length 369;  
Best Local Similarity 81.7%; Pred. No. 2,4e-130;

Matches 290; Conservative 37; Mismatches 28; Indels 0; Gaps 0;

```

QY 16 LIALALPAALAAASGRMMGIYVNASSTLITDSKSLQVLEPSTLITDSKRPRLPON 75
DB 15 ILAFSSLITLAVNNSGRMMGIYVNTSLITITKKNVQVLDPSQLITDSKRPRLPON 74
QY 76 PGLIHSVSGIQLQSAVRECKQKQFNNRNNCPAPRPHLFGKIVNPGCRETAIFAITSASY 135
DB 75 PGLIHSVSGIQLQSAVRECKQKQFNNRNNCPAPRPHLFGKIVNPGCRETAIFAITSASY 134
QY 136 THSVASCSGSESTGCTCDYRRPGPGPMHMGCCSNIDPGLFGLREFVDSGEGKGRDL 195
DB 135 THSVASCSGSESTGCTCDYRRPGPGDWMHMGCCSNIDPGLFGLREFVDSGEGKGRDL 194
QY 196 FLMLHNNAGRTTVESEMRQCKGMSGSCVTRTMPLPLAAVGVLRRDFDQASR 255
DB 195 YLMNRHNNAGRTTVESEMRQCKGMSGSCAVRTGMRLPLFRAYDQFLKDFDQASR 254
QY 256 VLYGNBSNRASRAELLLEPDDPAKRPSPHDLVEFEKSPNCTYSGLTAGTAGRAV 315
DB 255 VLYGNBSNRASRAVQTHLEPDRPHKRPSPQDLVFEFEKSPNCTYSGLTAGTAGRAV 314
QY 316 NSSSPALDGCGLCCGCGHRTTRQVTEKNCNTRKWCCHVSCNTHIRVHLECL 370
DB 315 NSSSPALDGCGLCCGCGHRTTRQVTEKNCNTRKWCCHVSCNTHIRVHLECL 369

```

# RESULT 5

Wnt-1 protein - zebra fish

C:Species: Brachydanio rerio (zebra fish)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Jul-1999

C:Accession: S15013

R:Molven, A.; Njolstad, P.R.; Fjose, A.

EMBO J. 10, 799-807, 1991

Altile: Genomic structure and restricted neural expression of the zebrafish wnt-1 (int-

A:Reference number: S15013; MIM:61184125; EMBL:2009859

A:Accession: S15013

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-370 <MDL>

A:Cross-references: GB:X58860; GB:X57301; NID:462556; PIDN:CAA1687.1; PID:9833600

A:Genetics:

A:Gene: wnt-1

C:Superfamily: int-1 transforming protein

Query Match 78.3%; Score 1595; DB 2; Length 370;  
Best Local Similarity 75.7%; Pred. No. 4.6e-124;

Matches 261; Conservative 47; Mismatches 41; Indels 2; Gaps 2;

```

QY 1 MGLMALPGWVSATLLALALPALAANSSGRMMGIYVNASSTLITDSKSLQVLEPS 60
DB 1 MGLMALPGWVSATLLALALPALAANSSGRMMGIYVNASSTLITDSKSLQVLEPS 59
QY 61 LMLSLKORRLTRONPGLIHSVSGIQLQSAVRECKQKQFNNRNNCPAPRPHLFGKIVN 129
DB 60 LMLSLKORRLTRONPGLIHSVSGIQLQSAVRECKQKQFNNRNNCPAPRPHLFGKIVN 119
QY 121 CRETAIFAITSAGVTHSVASCSGSESTGCTCDYRRPGPGDWMHMGCCSNIDPGLF 180
DB 120 CRETAIFAITSAGVTHSVASCSGSESTGCTCDYRRPGPGDWMHMGCCSNIDPGLF 179
QY 181 GREVDVSEGRGDLFLMLHNNAGRTTVESEMRQCKGMSGSCVTRTMPLPLAAVGVL 240
DB 180 GREVDVSEGRGDLFLMLHNNAGRTTVESEMRQCKGMSGSCVTRTMPLPLAAVGVL 239
QY 241 AVGDVLRKRFQDASRVLYGNBSNRAS-RAELLLEPDDPAKRPSPHDLVEFEKSPNF 299
DB 240 LVGDVLRKRFQDASRVLYGNBSNRASRAEDPRLLEPDRPHKRPSPQDLVFEFEKSPNF 299

```

```

QY 300 ITSGRLGATAGAACNSSPALDGCGLCCGCGHRTTRQVTEKNCNTRKWCCHVSCN 359
DB 300 ITSGRLGATAGAACNSSPALDGCGLCCGCGHRTTRQVTEKNCNTRKWCCHVSCN 359
QY 360 CTRFVLEHCL 370
DB 360 CTRFVLEHCL 370

```

# RESULT 6

Transforming protein int-1 precursor - African clawed frog

Alternate names: pxwt-1 protein

C:Species: Xenopus laevis (African clawed frog)

C>Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jun-1999

C:Accession: S02113; S41649

R:Nodtimmer, A.; Melnik, E.; Vertizier, P.; Kistner, K. P.; Destrée, O.

EMBO J. 17, 11-18, 1999

Altile: Isolation of the Xenopus homolog of int-1/c-myc and expression during de-

A:Reference number: S02113; MIM:6098373; EMBL:24114.2

A:Accession: S02113

A:Molecule type: mRNA

A:Residues: 1-371 <MDL>

A:Cross-references: EMBL:X13348; NID:465235; PIDN:CAA1549.1; PID:965236

R:Go, X.; Kojima, G.A.; Haerends, W.M.; Koster, J.G.; Destrée, O.H.J.

Oncogene 9, 57-58, 1994

Altile: Characterization of a functional promoter for the Xenopus wnt-1 gene in vivo

A:Reference number: S41649; MIM:64119599; EMBL:849426

A:Accession: S41649

A:Molecule type: DNA

A:Residues: 1-371 <MDL>

A:Cross-references: EMBL:X56845

C:Genetics:

A:Gene: int-1

C:Superfamily: int-1 transforming protein

C:Keywords: glycoprotein; oncogene; transforming protein

E1-19/Domains: signal sequence #status predicted <SIS>

E20-371/Product: transforming protein int-1 #status predicted <MAT>

E28-261/279,304,317,360/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 71.9%; Score 1463; DB 1; Length 371;

Best Local Similarity 70.0%; Pred. No. 3.6e-113;

Matches 261; Conservative 59; Mismatches 59; Indels 12; Gaps 5;

```

QY 1 MGLMALPGWVSATLLALALPALAANSSGRMMGIYVNASSTLITDSKSLQVLEPS 58
DB 8 LGLKTI---WV----LAFSLNLIYVNSGRMMGIYVNASSTLITDSKSLQVLEPS 59
QY 59 PSLQLSKORRLTRONPGLIHSVSGIQLQSAVRECKQKQFNNRNNCPAPRPHLFGKIVN 118
DB 50 PSLQLSKORRLTRONPGLIHSVSGIQLQSAVRECKQKQFNNRNNCPAPRPHLFGKIVN 118
QY 119 PGRERATFAITSAGVTHSVASCSGSESTGCTCDYRRPGPGDWMHMGCCSNIDPGL 178
DB 119 PGRERATFAITSAGVTHSVASCSGSESTGCTCDYRRPGPGDWMHMGCCSNIDPGL 178
QY 179 LGRFVDSGEGKGRDLFLMLHNNAGRTTVESEMRQCKGMSGSCVTRTMPLPLAAVGVL 238
DB 179 LGRFVDSGEGKGRDLFLMLHNNAGRTTVESEMRQCKGMSGSCVTRTMPLPLAAVGVL 238
QY 239 FGRFVDSGEGKGRDLFLMLHNNAGRTTVESEMRQCKGMSGSCVTRTMPLPLAAVGVL 298
DB 239 FGRFVDSGEGKGRDLFLMLHNNAGRTTVESEMRQCKGMSGSCVTRTMPLPLAAVGVL 298
QY 299 FGRFVDSGEGKGRDLFLMLHNNAGRTTVESEMRQCKGMSGSCVTRTMPLPLAAVGVL 358
DB 299 FGRFVDSGEGKGRDLFLMLHNNAGRTTVESEMRQCKGMSGSCVTRTMPLPLAAVGVL 358
QY 359 FGRFVDSGEGKGRDLFLMLHNNAGRTTVESEMRQCKGMSGSCVTRTMPLPLAAVGVL 370
DB 359 FGRFVDSGEGKGRDLFLMLHNNAGRTTVESEMRQCKGMSGSCVTRTMPLPLAAVGVL 371

```

## RESULT 7

A29650

wingless (wg) protein precursor - fruit fly (*Drosophila melanogaster*)

M:Alternate names: int-1 homolog (Dint-1)

C:Species: *Drosophila melanogaster*

C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #extl\_change 15-Jul-1999

C:Accession: A29650; S41671; S41157

C:Release1: F.; Schenemann, M.; Wagensat, E.; Farren, P.; Weigelt, D.; Nusse, R.

Cell 50: 649-657, 1987

A:Title: The *Drosophila* homolog of the mouse mammary oncogene int-1 is identical to the

A:Reference number: A29650; MID:8727328; PMID:3111720

A:Accession: A29650

A:Molecule type: mRNA

A:Residues: 1-468 &lt;VAN&gt;

A:Cross-references: JB:M1749; MID:9157765; FILN:AA4647.1; PID:9457769

R:Van den Heuvel, M.; Hartman-Samos, C.; Kluken-Smith, J.; Pettimon, N.; Nusse, R.

EMBO J. 12: 5293-5302, 1993

A:Title: Mutations in the segment polarity genes wingless and porcupine impair secretion

A:Reference number: S41671; MID:94085405; PMID:826272

A:Accession: S41671

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-468 &lt;VAN&gt;

A:Cross-references: S: Nady, L.M.; Carroll, S.

Nature 367: 460-463, 1994

A:Title: Conservation of wingless patterning functions in the short-germ embryos of Trib

A:Reference number: S41156; MID:94150623; PMID:8107804

A:Accession: S41157

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 101-468 &lt;NAG&gt;

A:Gene: FlyBase:wg

A:Cross-references: FlyBase:FBgn0094009

C:Superfamily: int-1 transforming protein

C:Keywords: glycoprotein

Query Match

Best Local Similarity

Matches 203; Conservative

45.7%; Pred. No. 1.1e-76;

43; Mismatches 69; Indels 109; Gaps

8;

Query

31 SGR-----WGQIVAVASSITL

Dh

30 SGRGROSMWGIKAVGEFNNI-----TPIWMDPAIHSTLRKQRLVADNMGVGLAVK 84

Qy

85 GLQSAVRECKWQFRRRNCPIT---APGHLFGKIVRGCRFAFPATASGTHSVAR 141

Dh

85 GAAUATSECHQDFNRKKNKSTNRSRGNLEFKIIVRGCRFETIYATISAAHTSIAR 144

Qy

142 SCSEGSIESITCDY--RRGR-----GGPDWIMWJGCSUNIDFGHLEGFEDVDSGE 189

Dh

145 ACSEGTIESITCDYSHQSRSPQANHAGSVAGVADWEMWJGCSUNIDFGHLEGFEDVDSGE 204

Qy

190 KGRDLFECLNHNAGRTVFSEMRQECRCHSGSCTVFTQWKLPTLEAVDYLROH 249

Dh

205 RGNLREKNNLNHNAGRAHVLAEMRQECRCHSGSCTVFTQWKLNFVINDNKAR 264

Qy

250 FDGASVVLKSN-----RGSNRSRAELT----- 272

Dh

265 FDGATVQVYNSTRATNALAPVSPNAGSNVSGNGLIPQSHVYGEFERMLNDMPD 324

Qy

273 -----PLEPEDPAHKRPPSP 286

Dh

325 ILLENSHPISKIHHPNMPSPNSLDAQOGGRNGRGRKHNHYFQOLPNPNEHKRPPS 384

Qy

287 HDLVFEKSPNCTIYSGRLTATNARCNSSPALGCGCLLQSGRHRITQVNTRCN 346

Dh

385 KDLVLYEFPSECEKNLRQGIIDTHGRQNETSLGAVGCGDLMTCGGYFRQDVVVERCA 444

Qy

347 CTFHMCQVAVSNCITHTVRLNEL 370

Dh

445 CTFHMCQVAVSNCITHTVRLNEL 468

## RESULT 8

transforming protein int-1 - fruit fly (*Drosophila melanogaster*)C:Species: *Drosophila melanogaster*

C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #extl\_change 16-Feb-1997

C:Accession: A31377

C:Release1: E.; Kiss, I.; Pitt, A.; Arsenian, S.; Ingvarsson, S.; Duvard, A.; Hamad

Proc. Natl. Acad. Sci. U.S.A. 85: 304-308, 1988

A:Title: *Drosophila* homolog of the murine int-1 proto-oncogene.

A:Reference number: A31377; MID:8627634; PMID:3125722

A:Accession: A31377

A:Molecule type: mRNA

A:Residues: 1-469 &lt;PEV&gt;

A:Gene: int-1

A:Cross-references: FlyBase:FBgn0094009

C:Superfamily: int-1 transforming protein

C:Keywords: glycoprotein; oncogene; transforming protein

C:Keywords: glycoprotein; oncogene; transforming protein (covariant) #status predicted

Query Match

Best Local Similarity

Matches 203; Conservative

49.0%; Score 998; DB 1; Length 469;

43.2%; Pred. No. 1.1e-74;

53; Mismatches 100; Indels 114; Gaps 10;

Query

10 WSAATLLALALPAALA-----ANSSCK-----WGQIVAVASSITL

Dh

5 YIVVICLALGSSSSISOVEGRKQKSGRGMWGIKAVGEFNNI-----TPIWMDPAIHSTLRKQRLVADNMGVGLAVK 119

Qy

61 L-QLLSKQRLIRKQNPGLIHVSQGIQSAVRECKWQFRRRNCPIT---APGHLFGK 116

Dh

60 IHTLRKQRLVADNMGVGLAVKQANLASECHQDFNRKKNKSTNRSRGNLEFKI 119

Qy

117 VNGCRFAFPATASGTHSVARSSEGSIECTCDY--RRGR-----GGPD 164

Dh

120 VDRGCRFETIYATISAAHTSIARACSEGTIESITCDYSHQSRSPQANHAGSVAGVADWEMWJGCSUNIDFGHLEGFEDVDSGE 179

Qy

165 WHMGCSUNIDFGHLEGFEDVDSGEKGRDLFECLNHNAGRTVFSEMRQECRCHSGSCTVFTQWKLPTLEAVDYLROH 224

Dh

180 WEGQCSUNIDFGHLEGFEDVDSGEKGRDLFECLNHNAGRTVFSEMRQECRCHSGSCTVFTQWKLPTLEAVDYLROH 239

Qy

225 GSCTVFTQWKLPTLEAVDYLROHFDGASV-----GNRSNRA 266

Dh

240 GSCTVFTQWKLPTLEAVDYLROHFDGASV-----GNRSNRA 266

Qy

257 -----LV-----GNRSNRA 266

Dh

300 GLTIPOSLVIGEERERMLNDMPDILLENSHPISKIHHPNMPSPNSLDAQOGGRNGRGRKHNHYFQOLPNPNEHKRPPS 320

Qy

267 SRAEL-----LKEPEDPAHKRPPSPHOLVFEKSPNCTIYSGRLTATNARCNSSPALGCGCLLQSGRHRITQVNTRCN 346

Dh

360 RGNLREKNNLNHNAGRAHVLAEMRQECRCHSGSCTVFTQWKLNFVINDNKAR 264

Qy

321 ALDGELLYSGRHRITQVNTRCNCTFHMCQVAVSNCITHTVRLNEL 370

Dh

420 GVDGGLMCCGRITRDEYVVDRCATTFHMCQVAVSNCITHTVRLNEL 468

Qy

267 SRAEL-----LKEPEDPAHKRPPSPHOLVFEKSPNCTIYSGRLTATNARCNSSPALGCGCLLQSGRHRITQVNTRCN 346

Dh

360 RGNLREKNNLNHNAGRAHVLAEMRQECRCHSGSCTVFTQWKLNFVINDNKAR 264

Qy

321 ALDGELLYSGRHRITQVNTRCNCTFHMCQVAVSNCITHTVRLNEL 370

Dh

420 GVDGGLMCCGRITRDEYVVDRCATTFHMCQVAVSNCITHTVRLNEL 468

Qy

267 SRAEL-----LKEPEDPAHKRPPSPHOLVFEKSPNCTIYSGRLTATNARCNSSPALGCGCLLQSGRHRITQVNTRCN 346

Dh

360 RGNLREKNNLNHNAGRAHVLAEMRQECRCHSGSCTVFTQWKLNFVINDNKAR 264

Qy

321 ALDGELLYSGRHRITQVNTRCNCTFHMCQVAVSNCITHTVRLNEL 370

Dh

420 GVDGGLMCCGRITRDEYVVDRCATTFHMCQVAVSNCITHTVRLNEL 468

## RESULT 9

developmental regulator wnt-4 - African clawed frog

C:Species: *Xenopus laevis* (African clawed frog)

C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #extl\_change 10-Nov-1995

C:Accession: A49146; C49764

C:Release1: L.L.; Lott, A.P.; Moon, R.T.

Development 115: 463-473, 1992

A:Title: Analysis of wnt-4 in embryos of *Xenopus laevis*: a put family member express

A:Reference number: A49146; MID:95048810; PMID:1425335

A:Accession: A49146

A:Molecule type: mRNA

A:Residues: 1-352 &lt;MG&gt;

A:Gene: int-1

A:Cross-references: FlyBase:FBgn0094009

C:Superfamily: int-1 transforming protein

C:Keywords: glycoprotein; oncogene; transforming protein

C:Keywords: glycoprotein; oncogene; transforming protein (covariant) #status predicted

Query Match

Best Local Similarity

Matches 203; Conservative

49.0%; Score 998; DB 1; Length 469;

43.2%; Pred. No. 1.1e-74;

53; Mismatches 100; Indels 114; Gaps 10;

Query

10 WSAATLLALALPAALA-----ANSSCK-----WGQIVAVASSITL

Dh

5 YIVVICLALGSSSSISOVEGRKQKSGRGMWGIKAVGEFNNI-----TPIWMDPAIHSTLRKQRLVADNMGVGLAVK 119

Qy

61 L-QLLSKQRLIRKQNPGLIHVSQGIQSAVRECKWQFRRRNCPIT---APGHLFGK 116

Dh

60 IHTLRKQRLVADNMGVGLAVKQANLASECHQDFNRKKNKSTNRSRGNLEFKI 119

Qy

117 VNGCRFAFPATASGTHSVARSSEGSIECTCDY--RRGR-----GGPD 164

Dh

120 VDRGCRFETIYATISAAHTSIARACSEGTIESITCDYSHQSRSPQANHAGSVAGVADWEMWJGCSUNIDFGHLEGFEDVDSGE 179

Qy

165 WHMGCSUNIDFGHLEGFEDVDSGEKGRDLFECLNHNAGRTVFSEMRQECRCHSGSCTVFTQWKLPTLEAVDYLROH 224

Dh

180 WEGQCSUNIDFGHLEGFEDVDSGEKGRDLFECLNHNAGRTVFSEMRQECRCHSGSCTVFTQWKLPTLEAVDYLROH 239

Qy

225 GSCTVFTQWKLPTLEAVDYLROHFDGASV-----GNRSNRA 266

Dh

240 GSCTVFTQWKLPTLEAVDYLROHFDGASV-----GNRSNRA 266

Qy

257 -----LV-----GNRSNRA 266

Dh

300 GLTIPOSLVIGEERERMLNDMPDILLENSHPISKIHHPNMPSPNSLDAQOGGRNGRGRKHNHYFQOLPNPNEHKRPPS 320

Qy

267 SRAEL-----LKEPEDPAHKRPPSPHOLVFEKSPNCTIYSGRLTATNARCNSSPALGCGCLLQSGRHRITQVNTRCN 346

Dh

360 RGNLREKNNLNHNAGRAHVLAEMRQECRCHSGSCTVFTQWKLNFVINDNKAR 264

Qy

321 ALDGELLYSGRHRITQVNTRCNCTFHMCQVAVSNCITHTVRLNEL 370

Dh

420 GVDGGLMCCGRITRDEYVVDRCATTFHMCQVAVSNCITHTVRLNEL 468

Qy

267 SRAEL-----LKEPEDPAHKRPPSPHOLVFEKSPNCTIYSGRLTATNARCNSSPALGCGCLLQSGRHRITQVNTRCN 346

Dh

360 RGNLREKNNLNHNAGRAHVLAEMRQECRCHSGSCTVFTQWKLNFVINDNKAR 264

Qy

321 ALDGELLYSGRHRITQVNTRCNCTFHMCQVAVSNCITHTVRLNEL 370

Dh

420 GVDGGLMCCGRITRDEYVVDRCATTFHMCQVAVSNCITHTVRLNEL 468

Qy

267 SRAEL-----LKEPEDPAHKRPPSPHOLVFEKSPNCTIYSGRLTATNARCNSSPALGCGCLLQSGRHRITQVNTRCN 346

Dh

360 RGNLREKNNLNHNAGRAHVLAEMRQECRCHSGSCTVFTQWKLNFVINDNKAR 264

Qy

321 ALDGELLYSGRHRITQVNTRCNCTFHMCQVAVSNCITHTVRLNEL 370

Dh

420 GVDGGLMCCGRITRDEYVVDRCATTFHMCQVAVSNCITHTVRLNEL 468

A: Experimental source: neurula stage embryos  
 A: Note: sequence extracted from NCBI backbone (NCBI:117112)  
 R: Christlan, J.L.; Gavin, B.J.; McMahon, A.P.; Moon, R.T.  
 Dev. Biol. 143: 230-234, 1991

A: Title: Isolation of cDNAs partially encoding four Xenopus Wnt-1/int-1-related proteins  
 A: Reference number: A49764; M0ID:91122437; PMID:1991549

A: Accession: C49764

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 262-295, 'H', 297-335 <CHR>

A: Cross-references: GB:M55055

C: Superfamily: int-1 transforming protein

Query Match 42.9%; Score 873.5; DB 2; Length 352;  
 Best Local Similarity 44.6%; Pred. No. 1,6e-64;

Matches 164; Conservative 62; Mismatches 121; Indels 21; Gaps 5;

QY 6 LIPGVSAITLLAALPALAANSSGHWGIVVASNTLTDKSLDLYLEPSLILS 65

DB 1 MPEFFRLSLMTLAVFSNNSN-----WLYLAKSSVSGISEETETKGP-----1 50

QY 66 RKQRLLRQNPGLIHSYSGLSQSAVECKWQFNRMRNCPA-PSPLRQKIVNRCRET 124

DB 51 QRCVQCKRNLVWQSVYRQCAIAEDQYQFNRMRNCSITLDGNVFKIIRGTIPA 110

QY 125 AFEPAITAGVTHSVASCSGSEISCTCYRFRHGGSGDMWGGCNDIDFGLGREF 184

DB 111 AFEPAITAGVTHSVTRACSSGDLKCKGDTVTYGVSPQGFWSGSDNLYGVAESQSF 170

QY 185 VDSGK---GRDLRFLNNHNEAGRTTSEMPDECKCHGSGSCTVTCWMLPTLA 241

DB 171 VDVRERKSGSSSALMNLNNEAGRAKALLNNMVEKCHGSGSCEVKTQWAMETFEK 230

QY 242 VDDVDFPEPCGASPLVLCNNGSRASPAELLLEETEPRAKPSHDLVEEKSPPCY 301

DB 231 VGNVLKEKEDATIEVEKTKIGTKY-----LVPAKSGPKHTEDLVLYDSPPDCH 283

QY 302 SGRLGTACTAGACNSSSPALDGCCLCGRHRTQVYTRCNCPTFRHWCHVSRNT 361

DB 284 DLKNGVLTGTGRDCKTKSKAIDGCELMCGDHTEVEIYERKNNHMCVEKQKQH 343

QY 362 HTRVLEHC 369

DB 344 KYVEHETC 351

RESULT 10

S41156

Wingless protein - red flour beetle (fragment)

C: Species: Tribolium castaneum (red flour beetle)

C: Date: 07-SEP-1994 #sequence\_revision 14-Apr-1996 #text\_change 16-Feb-1997

C: Accession: S41156

R: Nagy, L.M.; Carroll, S.

Nature 367, 460-463, 1994

A: Title: Conservation of wingless patterning functions in the short-term embryos of Tribolium

A: Reference number: S41156; M0ID:94150623; PMID:8107804

A: Accession: S41156

A: Status: not compared with conceptual translation

A: Molecule type: mRNA

A: Residues: 1-303 <NMG>

C: Genetics:

A: Genes: wg

C: Superfamily: int-1 transforming protein

C: Keywords: glycoprotein

Query Match 42.6%; Score 866.5; DB 2; Length 303;  
 Best Local Similarity 53.5%; Pred. No. 5.1e-64;

Matches 162; Conservative 39; Mismatches 61; Indels 41; Gaps 6;

QY 109 GPHLFGKIVNGCETAFIPATISAGVTHSVASCSGSEISCTD--YRRR-----GPGS 162

DB 1 GKMLFKIYDKRHETAFIATISAAVTHAARACSGSLDNCGETHYKGRPHVSGNG 50

QY 163 -----ELUMHGGCSTNIDFSLTRFVDSGKGRDLRHLNHNNEAGRTTSEMP 216

DB 61 GALAVDFEFGGCSNIFGTVSRFVDAERGRTTEKKNNANNEAGRAVYKLMQRO 120

QY 217 ECKCHWSGSCVTRTWMRLPTLAVDVLDRFDGASVYVQ--NPGSRA----- 266

DB 121 ECKCHWSGSCVTRTWMRLPTLAVDVLDRFDGASVYVQ--NPGSRA----- 266

QY 267 -----SRAPLIP-----LEPEDPAKPPSHDLVEEKSPPCYSGRLGT 307

DB 181 PLKANSNSTHRSKRENEKRYVQ-LKPNRPHKPPGRIKLIVYENSPPTEKNEKRL 240

QY 308 ACTATPACNSSSPALDGCCLCGRHRTQVYTRCNCPTFRHWCHVSRNCNHTPLH 367

DB 241 VGHTEHNTSMVGLDTLMDGRGRTQEVVFEKNCIEHWTVEVKTAVPRTKTIH 300

QY 368 ECT 470

DB 301 TCV 403

RESULT 11

A35532

Wnt-3A protein - mouse

C: Species: Mus musculus (house mouse)

C: Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999

C: Accession: A35532

R: Koelink, H.; Nusse, R.

Genes Dev. 5, 381-388, 1991

A: Title: Expression of two members of the Wnt family during mouse development. Testis

A: Reference number: A35532; M0ID:91160973; PMID:1610141

A: Accession: A35532

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 1-62, 82-84

A: Cross-references: GB:X76642; M0ID:955433; EMBL:066477.1; F01065434

C: Superfamily: int-1 transforming protein

Query Match 41.4%; Score 843.5; DB 2; Length 352;  
 Best Local Similarity 45.1%; Pred. No. 4.8e-62;

Matches 161; Conservative 59; Mismatches 11; Indels 11; Gaps 4;

QY 16 LALALALPALAANSSGHWGIVVASNTLTDKSLDLYLEPSLILS 75

DB 7 LVLVSLKQAL--GSTFTWMSLAVPGVSSL-----STGFLRQETLTPKALPFCRNV 59

QY 76 POLHSVSGDLSQSAVECKWQFNRMRNCPADP-HLFGKLYNP3-KETAFIPATISAG 134

DB 60 VEIMSVAEVGRKADIDQCHQFNRMRNCTTVNSLAIPGVLKATPFSAFVAHAIASAG 119

QY 135 VTHSVASCSGSEISCTCYRFRHGGSGDMWGGCNDIDFGLGREF 184

DB 120 VAFATPSCASALVQTSPLDGSPECKKQGRSELEHRSWVSEFALAKRKPRA 179

QY 195 RLMLNHNNEAGRTTSEMPDECKCHGSGSCTVTCWMLPTLA 241

DB 160 R5AMNHNNNEAGRAKALLNNMVEKCHGSGSCEVKTQWAMETFEK 239

QY 256 PVIYVNGSNVAPAELELEHFAKPPSHDLVEEKSPPCYSGRLGT 307

DB 240 EKVY---EKHRESWVETLKPRTYFKVPEKGLVLYTASIN-ELNPGTSGEFDHGT 296

QY 315 QNSSSGALDGCCLCGRHRTQVYTRCNCPTFRHWCHVSRNCNHTPLH 367

DB 297 QNVSNGIDGCLCGRHRTQVYTRCNCPTFRHWCHVSRNCNHTPLH 367

RESULT 12

A35503

Wnt-3 protein - mouse

C: Species: Mus musculus (house mouse)

C: Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 16-Jul-1999

C: Accession: A35503

R. Boelink, H. Wagenaar, E. Lopes da Silva, S. Nusse, R. Proc. Natl. Acad. Sci. U.S.A. 87, 4519-4523, 1990  
 A:Title: Wnt-3, a gene activated by proviral insertion in mouse mammary tumors, is homologous to the Drosophila wingless gene.  
 A:Reference number: A15503; MUID:9020407; PMID:2162045  
 A:Accession: A35503  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-355 <ROE>  
 A:Cross-references: GB:M32502; NID:q198428; PILEN:AA84109.1; PID:9293672  
 C:Superfamily: Int-1 transforming protein

Query Match 41.1% Score 843.5; DB 2; Length 355;  
 Best Local Similarity 46.0%; Pred. No. 4,8e-62;  
 Matches 155; Conservative 53; Mismatches 120; Indels 9; Gaps 3;

QY 34 MWGIVAVASTNLIDSKDQVLEPSLQLSRKPRTIRNGGIIHVSAGSLQAVREC 93  
 DB 26 MWSLALCOQYTLAS-----QPLCGSIGLVPRKQLFRNRYIEIMPVABEVKLGIDEC 80  
 QY 94 KWQRNRNRCNPTAPGR-HLEGKIYNGCRETAIFAITASGTHSVANSCEGIESCT 152  
 DB 81 QHQRGRNRCNCTIDSLAIFGVLKATRESAFHAIASQVAFVTRSCAEGSTTCG 140  
 153 CDYRRRPGGPPMHMGCSNDIDFGLRFRFVDSGEGKRIPELMLNNEAGRTVFS 212  
 DB 141 CDSHHRGPPEGGMKMGCSSEADPGVLYREFADARENRHRAISANKNNENAGSTIILD 200  
 QY 213 EMROECKMGSGSTVTCNMRPLTRAVGVLEPFTDASRVLYNGSNRARSAPELL 272  
 DB 201 HMKHCCKHGLSGSEVCTCMAAPDFRAIDGLDKDYSLSERV---EKHREKQVYE 257  
 QY 273 RLEPEDPAHPPSPHDLVYEFKSNFCTYSGRIGTAGTASAINSSPALLDCELLCGK 332  
 DB 258 TLRAKVALFKPPTFRDLVYENSNCENPETGFEIHRKTCNVTSHGIDCDLLCGK 317  
 QY 333 GHRTGRTKTEKNCNCTFHMKCHVSCNCRHTRVLEHC 369  
 DB 318 GHNTREKREKCMCFHMCQVSCQCRIRYDHTC 454

RESULT 13  
 Wnt-4 protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 19-Apr-1993 \*sequence\_revision 19-Apr-1993 \*text\_change 15-Jul-1999  
 C:Accession: G36470  
 R:Boelink, H.J.; McGahan, J.A.; McGahan, A.P.  
 Genes Dev. 4, 2319-2332, 1990  
 A:Title: Expression of multiple novel Wnt-1/Int-1-related genes during fetal and adult mouse development.  
 A:Reference number: A36470; MUID:91122634; PMID:2279700  
 A:Accession: G36470  
 Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-351 <GAV>  
 A:Cross-references: GB:M89797; NID:9202401; PILEN:AAA0566.1; PID:9202402  
 C:Superfamily: Int-1 transforming protein

Query Match 41.1% Score 836; DB 2; Length 351;  
 Best Local Similarity 44.6%; Pred. No. 2e-61;  
 Matches 160; Conservative 55; Mismatches 124; Indels 20; Gaps 4;

QY 14 TLLTALAALPALAANSSGRMWGIVAVASTNLIDSKSLVLEPSDLSRKPRLIR 73  
 DB 9 SLRLVFAVFAASASN-----WLYLAKLSVSGISEETGE-----KLKGLLQRYOMCK 58  
 QY 74 QNPGLHVSAGSLQAVRECQWQFNRRNRCNPTAPGPHLEKTIYNGCRETAIFATISA 133  
 DB 59 RNLEVDVSRGAQALIEGQYQFRRNRNRCNCTIDSLPVGKVVGTGTRAPAFYATISA 118  
 QY 134 GYTHSVARSGSGSIESCTDYRRRPGGPPMHMGCSNDIDGRLFGREPFDSGEGK 192  
 DB 119 GVAFATRASSGELKCGCDRTVHVSQGGPQWGSNDIAGVAFVSQFVDAVERSKG 178

QY 194 --DLFPLNHNNEAGRTVFSERCEKCGHSGSGSTVTCNMRPLTRAVGVLEP 250  
 DB 179 ASSSRALMLNNEAGRTVFSERCEKCGHSGSGSTVTCNMRPLTRAVGVLEP 248  
 QY 251 DGASRVLYNRCNNSNARSAPELLPEPDPARPPSPHDLVYEFKSNFCTYSGRIGTAG 310  
 DB 219 DGATEVERPRVSSAKA-----LVKRNQKRPHTDDVLEHNSCTKQDINSYLTGT 291  
 QY 311 AGACNSSSPALDCELLCGGRHRIQRTVTEKNCNCTFHMKCHVSCNCRHTRVLEHC 369  
 DB 292 KGRTCNKRISKAIDGELLDCGRGHIAQVELAERGCGRFHMCQVFCVYGLVEIHIC 350

RESULT 14  
 Wnt-4 protein precursor - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 21-Mar-1995 \*sequence\_revision 26-May-1995 \*text\_change 03-May-1996  
 C:Accession: J02451  
 R:Yoshida, H.; Ohuchi, H.; Nohno, T.; Fujiwara, A.; Tanba, N.; Kawakami, Y.; Noji, S.  
 Biochem. Biophys. Res. Commun. 203, 1581-1588, 1994  
 A:Title: Regional expression of the Wnt-4 gene in developing chick central nervous system.  
 A:Reference number: J02451; MUID:95032034; PMID:7945306  
 A:Accession: J02451  
 A:Molecule type: mRNA  
 A:Residues: 1-351 <YOS>  
 A:Cross-references: This protein is involved in segmentation of the embryo into the neuromere and somite.  
 C:Superfamily: Int-1 transforming protein

Query Match 46.9% Score 827; DB 2; Length 351;  
 Best Local Similarity 43.1%; Pred. No. 1.1e-60;  
 Matches 158; Conservative 64; Mismatches 121; Indels 24; Gaps 6;

QY 8 PGWVASTLLALALPALAANSSGRMWGIVAVASTNLIDSKSLVLEPSDLSR 67  
 DB 6 PEYFLSKLLILLIATFSANASN-----WLYLAKLSVSGISEETGE-----KLKGLICR 52  
 QY 68 QPRLIQRNGLIHVSAGSLQAVRECQWQFNRRNRCNPTAPGPHLEKTIYNGCRETA 127  
 DB 54 QVQMRKNEVDVSRGAQALIEGQYQFRRNRNRCNCTIDSLPVGKVVGTGTRAPAFY 112  
 QY 128 FATTSAGTHSVARSGSGSIESCTDYRRRPGGPP--DWHRVYSGVLEPFLGSEEV 185  
 DB 113 YAISSAGVAFATYACSGSLDCKGSD--RTVGGPRGQWGSNDIAGVAFVSQFVDA 170  
 QY 186 DSGEGRDL--RFLNMLHNNEAGRTVFSERCEKCGHSGSGSTVTCNMRPLTRAV 242  
 DB 171 DYVERSKGASSNRALMLNHNNEAGRTVFSERCEKCGHSGSGSTVTCNMRPLTRAV 230  
 QY 243 GVLVDRFEGASRVLYNRCNNSNARSAPELLPEPDPARPPSPHDLVYEFKSNFCTYS 302  
 DB 241 GNLVREKREGATEVDEGIESGIV-----LVKRNQKRPHTDELVYINSPPQUND 263  
 QY 403 GRIGTGTAQRACNSSSPALDCELLCGGRHRIQRTVTEKNCNCTFHMKCHVSCNCR 362  
 DB 284 LKNGVLTGYSRQCKTSKAIDGELLDCGRGHIAQVELAERGCGRFHMCQVFCVYGL 343  
 QY 343 TVRLHEC 369  
 DB 344 VVEIHIC 350

RESULT 15  
 A36828  
 wingless homolog Wnt-3A protein - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 01-Dec-1993 \*sequence\_revision 18-Nov-1994 \*text\_change 23-Feb-1997



C:Accession: A48828  
 R:Wolda, S.L.; Moody, C.J.; Moon, R.T.  
 Dev. Biol. 155, 46-57, 1993  
 A:Title: Overlapping expression of Xwt-3A and Xwt-1 in neural tissue of *Xenopus laevis*  
 A:Reference number: A48828; M0ID:99106336; PMID:8416844  
 A:Accession: A48828  
 A>Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-352 <WOL>  
 A:Note: sequence extracted from NCBI backbone (NCBI:121343)  
 C:Superfamily: Int-1 transforming protein

Query Match 40.4% Score 822.5; DB 2: Length 352;

Best Local Similarity 43.4%; Pred. No. 2,6e-60;

Matches 154; Conservative 57; Mismatches 133; Indels 11; Gaps 4;

```

QY 16 LLAALPAALANSSGRMWGIIVNASSINLTDSKSLQVLEPSLQLSRKORLFCN 75
   ||:| || ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
DB 7 LLIIGHVLAIPYI--WMSLAVQOQYSSLSGT----QPIPGITIPGLVAKQWRFQNY 59
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
QY 76 PGLHSVSGGLQSAVRECKMORNRNMCPTA--GGPHLGKIVNRGRETAFIFATTSAG 134
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
DB 60 MEIMPSVAAEVKIGIGECCHQRCRKNMTIVNUNLAIFGVLDKATRESAFVHAIASAT 119
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
QY 135 VTHSVAKSGSEGSIESCTCDYRRPGGPGPIHWMGGSNDIDFGRLGREYVDSGEKGRUY 194
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
DB 120 VAFVAVRSTAEISATIGCCTHKKGPGEQKWKQCSSEDMDEGSMVSRFPADARENKPOA 179
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
QY 195 FELMNLHNNEAGRTIVFSEMKQCEKQGMGSGCTVTCMMRLPTLPAVGVLRRHPPQAS 254
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
DB 180 RSMNRRHNNEAGRTISLDHRLKKCKHGLSGSCVKTQMSQPDGFVIGVLYLKKIKYDAS 239
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
QY 255 RVIYGNKSNRASPARELLRLPEPDAAHKPPSPHDLVYFEKSPRPTYSGRLGTAGTAGRA 314
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
DB 240 EMVY--EKHRESKQWETLRPYTFEKPPIERDLIYESSNPCEPNETGSGFGTRDRE 296
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
QY 315 CNSSPALDQCELLCGRGHRTQVTERCNCSTFWCHVSCFNCTHTVYLHEC 369
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
DB 297 CNVTSHTGCGCLCGCGGONTIEREKREKCHCIFHWGCVSGQCMRVYDVHTC 351
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|

```

Search completed: April 22, 2003, 16:42:15  
 Job time : 47 secs



	Matches	370: Conservative	0: Mismatches	0: Indels	0: Gaps
QY	1	MCWALLPFWVSATLILLALAPALAAANSSGRNMGIVNASTNLLTDSKLOTLEPS	60		
Db	1	MCWALLPFWVSATLILLALAPALAAANSSGRNMGIVNASTNLLTDSKLOTLEPS	60		
QY	61	LDLSSRKQRFILKQNPGLHSVSGLSQSAVRECKWQFRNRNWCPTAGFHLFGKIVRG	120		
Db	61	LDLSSRKQRFILKQNPGLHSVSGLSQSAVRECKWQFRNRNWCPTAGFHLFGKIVRG	120		
QY	121	CHETAFIFALTSAQVTHSVANSGSEGSIESCTDPRFRHGGJLWMMHGGSDNIDFGFLF	180		
Db	121	CHETAFIFALTSAQVTHSVANSGSEGSIESCTDPRFRHGGJLWMMHGGSDNIDFGFLF	180		
QY	181	GREEVUSGCHKGQGLFELMKNLHNEAERTTVSEKQFVNGCHMSVSTVTTCMLPLFLP	240		
Db	181	GREEVUSGCHKGQGLFELMKNLHNEAERTTVSEKQFVNGCHMSVSTVTTCMLPLFLP	240		
QY	241	AVGVLEBDPFDASAVLYGNRGSNPASRAELLPLEEPFAHKPPPHDLYVEFSKPNCT	300		
Db	241	AVGVLEBDPFDASAVLYGNRGSNPASRAELLPLEEPFAHKPPPHDLYVEFSKPNCT	300		
QY	301	YSGRLGAGYFAGACNNSPALDGCCLCCGKGRHTCTPVERKNTFPMNCHVSCNG	360		
Db	301	YSGRLGAGYFAGACNNSPALDGCCLCCGKGRHTCTPVERKNTFPMNCHVSCNG	360		
QY	361	THTRYLHECL 370			
Db	361	THTRYLHECL 370			
RESULT 2					
WNT1_MOUSE					
ID	WNT1_MOUSE	STANDARD:	PRT:	370	AA.
AC	P04426:				
DT	13-AUG-1987 (Rel. 05, Created)				
DT	13-AUG-1987 (Rel. 05, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	WNT1, proto-oncogene protein precursor.				
GN	WNT1 OR WNT-1 OR INT-1.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI	NCBI_TaxID:10090;				
LN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-C3H:				
RC	MEDLINE=85024897; PubMed=6091914;				
RA	Coyen A.V., Nusse R.;				
RT	Structure and nucleotide sequence of the putative mammary oncogene				
RT	Int-1: proviral insertions leave the protein-encoding domain				
RT	Intact.";				
AL	Cell 39:233-240(1984).				
LN	[2]				
RP	SEQUENCE FROM N.A.				
RC	MEDLINE=86310810; PubMed=9018519;				
RA	Fung Y.-K.T., Shackelford G.M., Brown A.M.C., Samuels G.S.,				
RA	Varnus H.E.;				
RT	Nucleotide sequence and expression in vitro of cDNA derived from				
RT	mRNA of Int-1, a provirally activated mouse mammary oncogene.";				
RT	Mol. Cell. Biol. 5:3337-3344(1985).				
LN	[3]				
RP	SEQUENCE FROM N.A.				
RC	MEDLINE=91122614; PubMed=2279700;				
RA	Gavin B.J., McMahon J.A., McMahon A.P.;				
RA	"Expression of multiple novel Wnt-1/Int-1-related genes during fetal				
RT	and adult mouse development.";				
RT	Genes Dev. 4:2319-2332(1990).				
LN	[4]				
RP	POSSIBLE FUNCTION				
RC	MEDLINE=90363290; PubMed=2402907;				
RA	Thomas K.R., Catefuchi M.R.;				
RT	Targeted disruption of the murine Wnt-1 proto-oncogene resulting in				

PT Severe phenomalities in midbrain and cerebellar development.".  
 R1 Mature 340:847-850(1993).  
 RN 15)  
 RP DEVELOPMENTAL STAGE.  
 RC STRAIN-CBA/CA; TISSUE-Embryo;  
 RX MEDLINE-87244126; PubMed-1594565;  
 RA Wilkinson D.G., Bailes J.A., McMahon A.P.;  
 R1 "Expression of the proto-oncogene int-1 is restricted to specific  
 R1 neural cells in the developing mouse embryo.".  
 R1 Cell 50:75-86(1987).  
 RN 16)  
 R1 TISSUE SPECIFICITY.  
 RC STRAIN-ICR.  
 RX MEDLINE-87244127; PubMed-3554566;  
 RA Shaktiorty G.K., Varmus H.E.;  
 R1 "Expression of the proto-oncogene int-1 is restricted to postmeiotic  
 R1 male germ cells and the neural tube of mid-gestational embryos.".  
 R1 Cell 50:89-95(1987).  
 CC 1)- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN  
 CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A  
 CC SIGNALING MOLECULE. EXP-CELLANT IN CNS DEVELOPMENT. IS LIKELY TO  
 CC SIGNAL OVER ONLY FEW CELL DIAPHERS. PROMINENT IN IFN IN THE  
 CC INDUCTION OF THE MESENCEPHALON AND CEREBELLUM. MAY PLAY A CRITICAL  
 CC ROLE IN THE MORPHOGENESIS OF THE NEURAL TUBE AND/ OR THE EARLY  
 CC STAGES OF CNS DEVELOPMENT.  
 CC 1)- SUBCELLULAR LOCATION: possibly secreted and associates with the  
 CC extracellular matrix.  
 CC 1)- TISSUE SPECIFICITY: TESTIS AND MID-GESTATIONAL EMBRYOS. IN THE  
 CC TESTIS, DETECTED ONLY IN POSTMEIOTIC GERM CELLS UNDERGOING  
 CC DIFFERENTIATION FROM ROUND SPERMATIDS INTO MATURE SPERMATOGA. IN  
 CC THE EMBRYOS, EXPRESSION IS RESTRICTED TO THE DEVELOPING CNS IN  
 CC REGIONS OF THE NEURAL TUBE OTHER THAN THE TELENCEPHALON.  
 CC 1)- DEVELOPMENTAL STAGE: ACCUMULATES THROUGHOUT THE NEURAL PLATE AT  
 CC THE ANTERIOR HEAD FOLDS OF THE 9 DAY EMBRYO BUT ONLY AT ITS  
 CC LATERAL FOLDS IN MORE POSTERIOR REGIONS. FOLLOWING NEURAL TUBE  
 CC CLOSURE, EXPRESSION IS RESTRICTED TO SPECIFIC REGIONS OF THE  
 CC DORSAL WALL OF THE BRAIN VENTRICLES AND SPINAL CORD, THE VENTRAL  
 CC WALL OF THE MIDBRAIN AND THE Diencephalon, AND THE LATERAL WALLS  
 CC OF THE NEUROEPITHELIUM AT THE MIDBRAIN-HINDBRAIN JUNCTION.  
 CC 1)- DISEASE: MANY MOUSE MAMMARY TUMORS INDUCED BY M-SPV MAMMARY TUMOR  
 CC VIRUS (MMTV) CONTAIN A PROVIRUS INTEGRATED INTO A HOST CELL REGION  
 CC WHICH HAS BEEN NAMED INT-1 (NOW WNT-1).  
 CC 1)- SIMILARITY: BELONGS TO THE WNT FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: K02593; AAA19321.1; -  
 CC EMBL: M11943; AAA19322.1; -  
 CC EMBL: A23447; TWSM1.  
 CC EMBL: B23447; TWSM1.  
 CC EMBL: A16470; A16470.  
 CC EMBL: M0159855; Wnt1.  
 CC MOD: M0159855; Wnt1.  
 CC INTERPRO: IPR000970; Wnt\_ortholog.  
 CC EMBL: PF00110; Wnt: 1.  
 CC PRINTS: PR01349; WNTPROTEIN.  
 CC SMART: SM00097; WNT1: 1.  
 CC PROSITE: PS00246; WNT1: 1.  
 CC KW Developmental protein; Proto-oncogene; Glycoprotein; signal.  
 CC SIGNAL 1 27  
 CC CHAIN 42 370 WNT-1 PROTO-ONCOGENE (POTENTIAL).  
 CC FT CARR-AMD 29 N-LINKED (GLYCNC. . . ) (POTENTIAL).  
 CC FT CARR-AMD 316 N-LINKED (GLYCNC. . . ) (POTENTIAL).  
 CC FT CARR-AMD 346 N-LINKED (GLYCNC. . . ) (POTENTIAL).  
 CC FT CARR-AMD 359 N-LINKED (GLYCNC. . . ) (POTENTIAL).  
 CC SEQUENCE 370 AA: 41085 MW: 02EEB231092531A40 CP:Y43.  
 Query Match 99.38; Score 2021; Db 1; Def 1; 270

Best Local Similarity 98.9%; Pred. No. 3,7e-169;  
Matches 366; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 MGWALPGWVSATLLALPAALAAAGSGRMGIVYVASTNLTDSKSLQLEPES 60
DB 1 MGWALPGWVSATLLALPAALAAAGSGRMGIVYVASTNLTDSKSLQLEPES 60
QY 61 LQLLSKRQRLIKONPGILHSVSGIQSAVRECKWQEFNRNMCPTAPRPHLPKIVNRG 120
DB 61 LQLLSKRQRLIKONPGILHSVSGIQSAVRECKWQEFNRNMCPTAPRPHLPKIVNRG 120
QY 121 CRETAFIFATISAVTSHVARSQSEGSIESCTCPYRRKRCQGDMDWGQSONIDQERLP 180
DB 121 CRETAFIFATISAVTSHVARSQSEGSIESCTCPYRRKRCQGDMDWGQSONIDQERLP 180
QY 181 GREFVUSGKGRDLRFMLNHNNEAGRTIVSEMRQCKCHGSGSGIVRTCKWRLPILK 240
DB 181 GREFVUSGKGRDLRFMLNHNNEAGRTIVSEMRQCKCHGSGSGIVRTCKWRLPILK 240
QY 241 AVGDVLRDFDGASRVLYGNKQSNRASFALLRLEPELPAHKPPSPHDLVFEKSPFCT 300
DB 241 AVGDVLRDFDGASRVLYGNKQSNRASFALLRLEPELPAHKPPSPHDLVFEKSPFCT 300
QY 301 YSRRLTGTAGTACRACNSSPALDCCGCGHRTCTCVTERCNCIFRMCHVSCRN 360
DB 301 YSRRLTGTAGTACRACNSSPALDCCGCGHRTCTCVTERCNCIFRMCHVSCRN 360
QY 361 THTRVLECL 370
DB 361 THTRVLECL 370

RESULT 3
WNTL_AMEBE
ID WNTL_AMEBE STANCAPO PRI: 369 AA.
AC P21551:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE WNT-1 protein precursor.
GN WNT-1.
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomidae;
OC Ambystoma.
OX NCBI_TaxID=8296;
XN 111
RP SEQUENCE FROM N.A.
RX MEDLINE=9108134; PubMed=2259633;
RA Busse U., Guay J., Sequin C.;
RT "Nucleotide sequence of a cDNA encoding wnt-1 of the Mexican axolotl
RT Ambystoma mexicanum.";
RL Nucleic Acids Res. 18:7439-7439(1990).
RN 121
RP ERRATUM.
RX MEDLINE=91204483; PubMed=2017393;
RA Busse U., Guay J., Sequin C.;
RL Nucleic Acids Res. 19:981-981(1991).
RN 131
RP CHARACTERIZATION.
RX MEDLINE=93285407; PubMed=8508949;
RA Busse U., Sequin C.;
RT "Molecular analysis of the Wnt-1 proto-oncogene in Ambystoma
RT mexicanum (axolotl) embryos.";
RL Differentiation 53:7-15(1993).
RN 141
RP -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
RP TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A
RP SIGNALING MOLECULE IMPORTANT IN CNS DEVELOPMENT. IS LIKELY TO
RP SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -1- DEVELOPMENTAL STAGE: EARLY BLASTULA UNTIL GASTULATION. BARELY
CC EXPRESSED DURING GASTULATION AND PRESENT AGAIN FROM NEURULATION
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CC UNTIL LATE EMBRYOGENESIS.
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: X65279; CAA84991.1;
DB FRL: S14724; S13722.
DB PIR: S14724; S13722.
DB TrEMBL: P46097; WNT-1.
DB Pfam: P46010; wnt1.1.
DB PRINTS: P01349; WNTPROTEIN.
DB SMART: SM00477; WNT1.1.
DB PROSITE: PS02461; WNT1.1.
DE Developmental protein; glycoprotein; signal.
KW SIGNAL.
FT CHAIN 1;
FT CARRHYD 20; 369; N-LINKED (GLCNAC...); (POTENTIAL).
FT CARRHYD 28; 277; N-LINKED (GLCNAC...); (POTENTIAL).
FT CARRHYD 315; 315; N-LINKED (GLCNAC...); (POTENTIAL).
FT CARRHYD 358; 358; N-LINKED (GLCNAC...); (POTENTIAL).
SQ SEQUENCE 369 AA; 41384 MW; DC215A620F619421 75.44;

Query Match 42.1%; Score 1671; DB 1; Length 369;
Best Local Similarity 41.7%; Pred. No. 1.3e-194;
Matches 290; Conservative 37; Mismatches 28; Indels 0; Gaps 0;

QY 16 LIALALPAALAAAGSGRMGIVYVASTNLTDSKSLQLEPESLTSKQRLIKON 75
DB 16 LIALALPAALAAAGSGRMGIVYVASTNLTDSKSLQLEPESLTSKQRLIKON 75
QY 15 ILAFSSLTNTAAVNSGIRMGVNVVITSLDITKQVQVLTFLQSLSKQRLIKON 74
DB 15 ILAFSSLTNTAAVNSGIRMGVNVVITSLDITKQVQVLTFLQSLSKQRLIKON 74
QY 76 FGLHNSVSLQSAVRECKWQEFNRNMCPTAPRPHLPKIVNRG 135
DB 76 FGLHNSVSLQSAVRECKWQEFNRNMCPTAPRPHLPKIVNRG 135
QY 75 POLLRSLNSQGLSKMRCKWQEFNRNMCPTAPRPHLPKIVNRG 134
DB 75 POLLRSLNSQGLSKMRCKWQEFNRNMCPTAPRPHLPKIVNRG 134
QY 136 TRSVARSQSEGSIESCTCPYRRKRCQGDMDWGQSONIDQERLP 195
DB 136 TRSVARSQSEGSIESCTCPYRRKRCQGDMDWGQSONIDQERLP 195
QY 135 TRSVARSQSEGSIESCTCPYRRKRCQGDMDWGQSONIDQERLP 194
DB 135 TRSVARSQSEGSIESCTCPYRRKRCQGDMDWGQSONIDQERLP 194
QY 196 FLNHLNNEAGRTIVSEMRQCKCHGSGSGIVRTCKWRLPILK 255
DB 196 FLNHLNNEAGRTIVSEMRQCKCHGSGSGIVRTCKWRLPILK 255
QY 195 YLNNPNNAGRTIVSEMRQCKCHGSGSGIVRTCKWRLPILK 254
DB 195 YLNNPNNAGRTIVSEMRQCKCHGSGSGIVRTCKWRLPILK 254
QY 256 VLYGNQSNRASFALLRLEPELPAHKPPSPHDLVFEKSPFCT 315
DB 256 VLYGNQSNRASFALLRLEPELPAHKPPSPHDLVFEKSPFCT 315
QY 255 VLYGNQSNRASFALLRLEPELPAHKPPSPHDLVFEKSPFCT 314
DB 255 VLYGNQSNRASFALLRLEPELPAHKPPSPHDLVFEKSPFCT 314
QY 316 NSSSFLQGLTQSPHPTPOVTERCNCIFRMCHVSCRN 370
DB 316 NSSSFLQGLTQSPHPTPOVTERCNCIFRMCHVSCRN 370
QY 315 NSSSFLQGLTQSPHPTPOVTERCNCIFRMCHVSCRN 369
DB 315 NSSSFLQGLTQSPHPTPOVTERCNCIFRMCHVSCRN 369

RESULT 4
WNTL_AMEBE
ID WNTL_AMEBE STANCAPO PRI: 370 AA.
AC P24257:
DT 01-MAR-1991 (Rel. 41, Created)
DT 01-MAR-1991 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Wnt-1 protein precursor.
GN WNT1 OR WNT-1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
XN 111
RP SEQUENCE FROM N.A.
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RX MEDLINE=9114425; PubMed=2709859;
RA Molven A., Njolstad P.R., Fjose A.;
RT "Genomic structure and restricted neural expression of the zebrafish
RT wnt-1 (int-1) gene."
RL EMBL J. 10:799-807(1993).
CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A
CC SIGNALING MOLECULE IMPORTANT IN CNS DEVELOPMENT. IS LIKELY TO
CC SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
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CC
DR EMBL: X58880; CAA11687.1; -.
DR EMBL: X58881; CAA11687.1; JOINED.
DR EMBL: X58882; CAA11687.1; JOINED.
DR EMBL: X58883; CAA11687.1; JOINED.
DR PIR: S15013; S15013.
DR ZFIN: ZDB-GENE-980526-526; wnt1.
DR InterPro: IPR000970; Wnt_glycocalyx.
DR Pfam: PF00110; wnt; 1.
DR PRINTS: PR01349; WNTPROTEIN.
DR SMART: SM00097; WNT1; 1.
DR PROSITE: PS00246; WNT1; 1.
KM Developmental protein; glycoprotein; signal.
FT SIGNAL.
FT CHAIN.
FT CARBOHYD. 28 370 N-1-PROTEIN.
FT CARBOHYD. 316 316 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD. 359 359 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 370 AA: 41010 MW: F2AB0A82DB931D3E CRC64:

Query Match 78.3%; Score 1595; DB 1; Length 370;
Best Local Similarity 75.7%; Pred. No. 5,9e-132;
Matches 281; Conservative 47; Mismatches 41; Indels 2; Gaps 2;

QY 1 MGMLALPROMWSATILLALALPAALAAANSGRMWGIIVNVAASNTLITSKSLQVLEPS 60
DB 1 MRVALLELA-VKAAVCVLLVSSLTGTCAVNNSGRMWGIIVNVAASGNLLITNSKNVQVLDPS 59
QY 61 LQLLSKORRLIRQNGIILHSVSQGLSAVRECKWGFENRPMKPTAPGPHELEKIVNRG 120
DB 60 LALLSRQKRLIRQNGIILHSVSQGLSAVRECKWGFENRPMKPTAPGPHELEKIVNRG 119
/ 121 CRETAFLFAITAGVTHVAASCSSEISCTCDYRRRGPGCDWHMGCCSNIDGRLF 180
DB 120 CRETAFLFAITAGVTHVAASCSSEISCTCDYRRRGPGCDWHMGCCSNIDGRLF 179
QY 181 GRETVSGEGRDLRFILNLHNEAGRTVFESMEQEKCKGNSGCTVRIQWMLPLR 240
DB 180 GRETVSGEGRDLRFILNLHNEAGRTVFESMEQEKCKGNSGCTVRIQWMLPLR 239
QY 241 AVGVCLDRFDGASRYLYGNRGNRAS-PAELLR-LEPDPAHAPSPFHDVLYFEKSPNFC 299
DB 240 LVGVCLDRFDGASRYLYGNRGNRAS-PAELLR-LEPDPAHAPSPFHDVLYFEKSPNFC 299
QY 300 TYSGRGLTAGTAGRACNSSSPALDGCCLCGRGKRTTORVEKNCNCFHMCVSTRN 359
DB 300 TYSGRGLTAGTAGRACNSSSPALDGCCLCGRGKRTTORVEKNCNCFHMCVSTRN 359
QY 360 CTHRTVHECT 370
DB 360 CTHRTVHECT 370

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RESULT 5
WNT1_XENLA
AC WNT1_XENLA STANDARD; PRT; 371 AA.
ID P10108;
DI 01-MAR-1989 (Rel. 10, Created)
DI 01-MAR-1989 (Rel. 10, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE WNT-1 protein precursor (XWNT-1) (XINT-1).
GN WNT-1 OR INT-1. (African clawed frog).
OS Xenopus laevis (African clawed frog); Vertebrata; Eumetazoa;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89098373; PubMed=2911462;
RA Norrmeier J., Meljlik F., Verttjer P., Rijsević E. Oestre O.;
RT "Isolation of the Xenopus homolog of int-1/wingless and expression
RT during neurula stages of early development."
RL Nucleic Acids Res. 17:11-18(1989).
RN [2]
RP FUNCTION.
RX MEDLINE=89376559; PubMed=2673541;
RA Molven A.P., Moon R.T.;
RT "Genomic structure and expression of the proto-oncogene int-1 in xeno-pus embryos
RT leads to duplication of the embryonic axis."
RL Cell 58:1197-1204(1989).
CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A
CC SIGNALING MOLECULE IMPORTANT IN CNS DEVELOPMENT. IS LIKELY TO
CC SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -1- TISSUE SPECIFICITY: AT NEURULA IN ANTERIOR NEURAL FOLD. AT TAILBU
CC IN DORSAL MIDLINE OF MIDBRAIN.
CC -1- DEVELOPMENTAL STAGE: NEURULA ONWARDS.
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
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CC
DR EMBL: X13138; CAA31528.1; -.
DR PIR: S02113; TXNT1.
DR InterPro: IPR000970; Wnt_glycocalyx.
DR Pfam: PF00110; wnt; 1.
DR PRINTS: PR01349; WNTPROTEIN.
DR SMART: SM00097; WNT1; 1.
DR PROSITE: PS00246; WNT1; 1.
KM Developmental protein; glycoprotein; signal.
FT SIGNAL.
FT CHAIN.
FT CARBOHYD. 28 371 N-1-PROTEIN.
FT CARBOHYD. 261 261 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD. 317 317 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD. 360 360 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 371 AA: 41125 MW: 1FAC44F5F0CB4B72 CF74;

Query Match 71.9%; Score 1463; DB 1; Length 371;
Best Local Similarity 70.0%; Pred. No. 2e-120;
Matches 261; Conservative 50; Mismatches 50; Indels 12; Gaps 5;

QY 1 MGMLALPROMWSATILLALALPAALAAANSGRMWGIIVNVAASNTLITSKSLQVLE 54
DB 8 LGKLT-...-WV-...-LAFSSLSNTIAVNNSGRMWGIIVNVAASNTLITSKSLQVLE 59
QY 59 FSLQLSKORRLIRQNGIILHSVSQGLSAVRECKWGFENRPMKPTAPGPHELEKIVN 118

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DB 60 PSGLISR<OKHLRQNPGLISITIGLHSAIRCKHFFNRNMCPTGTCNVFGKTLN 118  
 QY 119 RGCRETAFIFATTSAGVTHSVARSCEGSIESTCTCDYRPRGPGDGMHMGCCSNDIDPR 178  
 DB 119 RGCRETAFIFATTSAGVTHSVARSCEGSIESTCTCDYRPRGPGDGMHMGCCSNDIDPR 178  
 QY 179 LFRFVDSGEGKDLRFMLNHNAGTTVSEMGCEKCGMGSSTYRTWMLT 238  
 DB 179 FIFRFVDSGEGKDLRFMLNHNAGTTVSEMGCEKCGMGSSTYRTWMLT 238  
 QY 239 LRAVGVLEDRFDGASRYLYNGRSNR-ASRAELLRLPEPDPAHKRPSFHDLYFEKSPN 247  
 DB 239 FRSVGFALKDRFDGASKVLYTSNNGSRNMGSRDPPHLEPENPTHALPSQDLYFEKSPN 248  
 QY 298 FCTYSGRGTACTAGACRACSSPALDGCCLCCGRSHRTPTQVTERECNTEFHMCQVSC 357  
 DB 298 FCTYSGRGTACTAGACRACSSPALDGCCLCCGRSHRTPTQVTERECNTEFHMCQVSC 357  
 QY 358 RNCSTHRLVLETL 370  
 DB 359 LNCSTHRLVLETL 371

## RESULT 6

WNT1\_BOIMO STANDARD: PRT: 39% AA.  
 AC P49340;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Wnt-1 protein precursor.  
 GN Wnt-1.  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
 OC Diptera; Bombycoidea; Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Amaratilaka, Hui C., Kokubo H., Dero K., Suzuki Y.;  
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBD databases.  
 CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN  
 CC TRANSMEMBRANE RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.  
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 CC -----  
 DR EMBL: D14167; BAA0211.1;  
 DR InterPro: IPR000970; Wnt\_gthfactor.  
 DR Pfam: PF00110; wnt.1.  
 DR PRINTS: PR01349; WNTPROTEIN.  
 DR SMART: SM00097; WNT1.1.  
 DR PROSITE: PS02246; WNT1.1.  
 KW Developmental protein; Glycoprotein; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 392 WNT-1 PROTEIN.  
 FT CARBOHYD 99 99 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 338 338 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 368 368 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 392 AA: 44204 MW: E25BFE210F44D6 CRC64:

Query Match 52.28; Score 1063.5; DB 1; Length 392;  
 Best Local Similarity 56.36; Pred. No. 166-85;  
 Matches 205; Conservative 39; Mismatches 91; Indels 29; Gaps 8;  
 QY 34 WGVIVNASTNLTDSKSLDVLPSLQ-LISRPKRPFLIRQNPGLHVSGLQSAVRE 92

## RESULT 7

WNT3\_DROME STANDARD: PRT: 44% AA.  
 ID WNT3\_DROME  
 AC P06151; Q27069; Q27069; Q27069;  
 DT 01-MAR-1996 (Rel. 10, Created)  
 DT 01-MAR-1996 (Rel. 10, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein INT-1 precursor (WNT-1) (Wingless protein).  
 GN Wnt-1.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Ephydroptera;  
 OC Muscomorpha; Ephydroptera; Drosophilidae; Drosophila.  
 OX Wnt-1; TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE:8-723528; PubMed:111726;  
 RA Rijsewijk F., Schweinmann M., Wagenaar E., Patten J., Weigel D.,  
 RA Nusse R.;  
 RL "The Drosophila homolog of the mouse mammary cell-specific Int-1 is  
 RL identical to the segment polarity gene wingless".  
 RL Cell 50:649-657(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE:8220634; PubMed:4129722;  
 RA Duvicourt E., Kils J., Patti A., Arsonian S., Jaiswal M. S.,  
 RA Duvicourt A., Hamada M., Klein G., Suemmel J.;  
 RL "Protophila homolog of the murine Int-1 protein is...".  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:3034-3038(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A. AND MUTANTS.  
 RA MEDLINE:94085405; PubMed:8262972;  
 RA van den Heuvel M., Barryman-Samos C., Klingenstein J., Perrimon N.,  
 RA Nusse R.;  
 RL "Mutations in the segment polarity genes wingless and porcupine  
 RL impair secretion of the wingless protein".  
 RL EMBO J. 12:5293-5302(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=Berkeley;  
 RA MEDLINE:20196006; PubMed:10731132;  
 RA Adams M.C., Pelinaker S.E., Holt R.A., Evans C.A., Joyner J.D.,  
 RA Amaratilaka H., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sifton G.G., Wortman J.F., Yarden J., Zhang J., Chen L.X.,

RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champagne M., Pfeiffer M.C.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos L.G.,  
 Rall J.F., Abayanti A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolintinas S.,  
 Borokova D., Botchan M.R., Bouck J., Brackstein P., Brothier P.,  
 Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 de Pablos B., Delcher A., Deng Z., Dey M.A.D., Dew I., Dietz S.M.,  
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Hartis N.L., Harvey D., Heiman T.J., Heintz J.R., Hewick J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,  
 Jalali M., Kalish J., Karpen G.H., Ke Z., Kemson J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Maltsev B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,  
 Palazolo K., Pittman G.S., Pan S., Pollard J.D., Puri V., Reese M.G.,  
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao C.A.,  
 Ye J., Yen R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou M., Zhu S., Zhu X., Zhu H.O.,  
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 "The genome sequence of *Drosophila melanogaster*."  
 Science 287:2185-2195(2000).  
 [5]  
 RA SECRETION.  
 RP MEDLINE:90358657; PubMed:2582493;  
 RA van den Heuvel M., Nusse R., Johnston P., Lawrence P.A.;  
 RT "Distribution of the wingless gene product in *Drosophila* embryos: a  
 RL protein involved in cell-cell communication."  
 Cell 59:739-749(1989).  
 RN [6]  
 RN PHOSPHORYLATION OF ARM.  
 RP MEDLINE:95113174; PubMed:7529201;  
 RA Pelletier M., Pal L.M., Casey M.;  
 RT "Phosphorylation of the *Drosophila* adherens junction protein  
 RL Armadillo: roles for wingless signal and zeste-white 3 kinase."  
 Dev. Biol. 166:543-556(1994).  
 RN [7]  
 RN PROTEIN INTERACTION WITH WG AND EN.  
 RP TISSUE-Embryo;  
 MEDLINE:93113685; PubMed:1335365;  
 A Siegfried E., Chou T.B., Perrimon N.;  
 RT "Wingless signaling acts through zeste-white 3, the *Drosophila* homolog  
 RL of glycogen synthase kinase-3, to regulate engrailed and establish  
 RL cell fate."  
 Cell 71:1167-1179(1992).  
 CC -1- FUNCTION: Segment polarity protein. Binds to the *frizzled* seven-  
 CC transmembrane receptors. This protein is probably a growth factor.  
 CC Acts on neighboring cells to regulate at least one gene, the  
 CC homeobox segmentation gene engrailed. Wg signaling represses arm  
 CC phosphorylation. Wg signaling operates by inactivating the *sgg*  
 CC repression of engrailed autoactivation.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.  
 CC  
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CC EMBL: M17230; AAA28647.1;  
 DR EMBL: J03650; AAA28646.1;  
 DR EMBL: S67382; AAB29368.1;  
 DR EMBL: S67343; AAB29369.1;  
 DR EMBL: AE003617; AAP2501.1;  
 DR PIR: A11317; IYFTH1.  
 DR PIR: A29650; A29650.  
 DR Flybase: FBgn004009; wg.  
 DR InterPro: IPR000970; wnt\_gtfactor.  
 DR Pfam: PF00110; wnt1\_1.  
 DR PRINTS: PR01349; WNTPROTEIN.  
 DR SMART: SM00097; WNT1; 1.  
 DR PROSITE: PS00246; WNT1; 1.  
 KW Developmental protein; glycoprotein; Segmentation polarity protein;  
 KW Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 466 PROTEIN INT-1.  
 FT CARBOHYD 103 103 N-LINKED (GLUCNA... ) (POTENTIAL).  
 FT CARBOHYD 106 106 N-LINKED (GLUCNA... ) (POTENTIAL).  
 FT VARIANT 414 414 C -> S (IN ALLELE WS-11114).  
 FT VARIANT 104 104 G -> D (IN ALLELE WS-11114).  
 FT VARIANT 221 221 W -> C (IN REF. 2).  
 FT CONFLICT 182 182 G -> D (IN ALLELE WS-11114).  
 FT CONFLICT 204 204 N -> T (IN REF. 2).  
 FT CONFLICT 275 275 N -> T (IN REF. 2).  
 FT CONFLICT 297 297 G -> A (IN REF. 2).  
 FT CONFLICT 315 315 E -> EE (IN REF. 2).  
 FT CONFLICT 364 364 K -> N (IN REF. 2).  
 FT CONFLICT 391 391 E -> D (IN REF. 2).  
 FT CONFLICT 441 441 E -> D (IN REF. 2).  
 SQ SEQUENCE 468 AA: 51946 MW: 766972A71E6171 3F774  
 Query Match 50.2% Score 1022.5 DB 1: Growth 408;  
 Best Local Similarity 45.7% Prod. No. 76e82;  
 Matches 203; Conservative 43; Mismatches 86; Indels 106; Gaps 8;  
 QY 31 SRR-----WAGYVNASSTNLLTTSKLSQLEPST--QLLSKQ4P41P2NPGILHSVG 64  
 DB 30 SSGGSGSMWGIKAKVEPNNI-----TPYWKDPAHSTLRKQFPLVYKNPVGLAVK 84  
 QY 85 GDSAVRECKWQFRNRKNCPT---ATGPHLPKIVNKGCRATATFATTSAGCTHSYAR 141  
 DB 85 GANLAISSQHQFRNRKNCPTSTFNSSKRLPKIYDRGCEITFYIAA;SAAVHSTAP 144  
 QY 142 SSSSESTLESITCY--RRRGF-----GGTFHWKGGSDN;CH RPLQHEVDGAE 189  
 DB 145 ACSSEGTLESTCYSHQSRSPQANHQAQSVAGVDEWGGSDN;CH RKFSEFVDGGE 204  
 QY 190 KGRDIFRLMNLHNEAARTIVSEKQEGKQSGNSCTVTRTQWKR;CHILFAYGDLKR 249  
 DB 205 KGRNLFRKMLHNEENGRHAYQAEKQEGKQSGNSCTVTRTQWKR;CHLFRVIGDLKAR 264  
 QY 250 FQASRVLYGN-----KQSRASRAELL----- 272  
 DB 265 FQATRVQVINSLRATNALAPVSNAAASMSVGSNLLIPQSVYVLEELERMLNDMP 344  
 QY 273 ----- 344  
 DB 326 ILLENSHPIKIHHPMPSPNSIPQADRGGRGRQCKINRHEFLNLHNEHKPPDS 364  
 QY 287 HOLVTFEKSINPTYSQKQGTAGACACSSSPALDGLCCS;CHSTFQVTECN 346  
 DB 385 KDLVLEPSISPEFKLRQGLIGIHGRQNETSLGVDGGLMCGSRHPRFEVYVERGA 444  
 QY 347 CTFHWGVSTFRCTHIVLECH 370  
 DB 445 CTFHWGVSTFRCTHIVLECH 468  
 RESULT 8  
 WNA\_MOUSE  
 ID WNA\_MOUSE STANDARD: PRT: 352 AA.

```

AC P27467
DT 01-AUG-1992 (rel. 23, Created)
DT 01-AUG-1992 (rel. 23, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE WNT-3A protein precursor.
GN WNT3A OR WNT-3A
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=9150971; PubMed=2001840;
RA Roelink H., Nusse R.;
RT *Expression of two members of the Wnt family during mouse
RT development -- restricted temporal and spatial patterns in the
RT developing neural tube.*
RL Genes Dev. 5:381-384(1991).
CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS. WNT-3 AND WNT-3A PLAY DISTINCT ROLES IN
CC CELL-CELL SIGNALING DURING MORPHOGENESIS OF THE DEVELOPING NEURAL
CC TUBE.
CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -1- TISSUE SPECIFICITY: DORSAL PORTION OF THE NEURAL TUBE (DEVELOPING
CC ROOF PLATE). AND MESENCHYME TISSUE SURROUNDING THE EMBLIAL
CC VEINS.
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56842; CAA0173.1;
DR PIR: A39532; A39532;
DR MGD: M0198956; Wnt3a.
DR InterPro: IPR000970; Wnt_grtfactor.
DR Pfam: PF00110; Wnt1.
DR PRINTS: PR01349; WNTPROTEIN.
DR SMART: SM00977; WNT1.1.
DR PROSITE: PS00245; WNT1.1.
KW Developmental protein; Glycoprotein; Signal; Extracellular matrix.
FT SIGNAL 1 24
FT CHAIN 25 352 WNT-3A PROTEIN.
FT CARBOHYD 87 87 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 352 AA: 39257 MW: 74DFCSH3BA8EF63 CRC64:

Query Match 41.4% Score 843.5 DB 1: Length 352:
Best Local Similarity 45.4% Pred. No. 2,4e+66:
Matches 161: Conservative 53: Mismatches 110: Indels 11: Gaps 4:

QY 16 LTAALPAALAASSGRBMWGIYVAVASTNLTLDKSLQVLEPSDILSRKQRLIPON 75
DB 7 LILVLSLKOAL--GSPYIWMSTAVAGPOYSSTL-----STQPLTLASIPGLVPKQLDFCHNY 59
QY 76 PELLHSVSGLSAVRECKWQFBNRBNWCTATGP-HLEGGIVAGRGREAFAPITASG 134
DB 60 VEIMSVAEQVKKAGIOECHOHPRGRNKCITTSNSALIFGVYLKAKREAYAHAIASNG 119
QY 135 VTHSVASCSGSESTGCTDYRRKPGGPDMMWGGCSNDIFGLFGREFVDSGCKGDI 194
DB 120 VAFATVTRSCAEGSAALICGSSRLGSPGEGMKWGSDEIDIEFGGVMSREFADAREPDA 179
QY 195 PELMLTHNNEAGRTVTFSEMRQCKGMSGCTVATCMRLPTLRAVGVVLDRPDGAS 254
DB 180 RAAKMHNNENAGROALIASHMLKCKCHGLSGCEVATCMWQSPDPRFTIGPLKDKYDSAS 239

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QY 255 KVLQNGRGSNFAASVELLRLPEEDPAHKPPSPHDLYVERKSPANCYSGRLCTAGTGRA 314
DB 240 EMVY---EKHRSKQWETLRLPRPYTFKVPTEEDLYVYFAFSPNCFENETSDPDT 295
QY 315 CNSSSPALGCELLACGGHGRHRTQRTQVTEKCNTPHMCYVSPNTHFRVYHHC 369
DB 297 CWSNHSHTGCDLLVGGHGNATFRKRCRCHCFHMCYVSPNTHFRVYHHC 351

RESULT 9
WNT3_MOUSE
ID WNT3_MOUSE STANDARD PRT: 355 AA.
AC P17553;
DT 01-AUG-1992 (rel. 15, Created)
DT 01-AUG-1992 (rel. 15, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE WNT-3 protein oncogene protein precursor.
GN WNT3 OR WNT-3 OR INT-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=924907; PubMed=2102045;
RA Roelink H., Megenard D., Lopez Ja Silva S., Nusse R.;
RT *Wnt-4, a gene activated by proviral insertion in mouse mammary
RT tumors, is homologous to int-1/Wnt-3 and is transiently expressed in
RT mouse embryos and adult brain.*
RL Proc. Natl. Acad. Sci. U.S.A. 97:4519-4523(1999)
CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS. WNT-3 AND WNT-3A PLAY DISTINCT ROLES IN
CC CELL-CELL SIGNALING DURING MORPHOGENESIS OF THE DEVELOPING NEURAL
CC TUBE.
CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -1- TISSUE SPECIFICITY: DORSAL PORTION OF THE NEURAL TUBE, DORSAL
CC ECTODERM, THE BRANCHIAL ARCHES, AND THE LIMB BUDS.
CC -1- DISEASE: SOME MOUSE MAMMARY TUMORS INDUCED BY MOUSE MAMMARY TUMOR
CC VIRUS (MMTV) CONTAIN A PROVIRUS INTEGRATE IN A HOST CELL WHICH
CC WHICH HAS BEEN NAMED WNT-3.
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC -----
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CC -----
DR EMBL: M32502; AAB38109.1;
DR PIR: A35502; A35503;
DR MGD: M0198953; Wnt3.
DR InterPro: IPR000970; Wnt_grtfactor.
DR Pfam: PF00110; Wnt1.
DR PRINTS: PR01349; WNTPROTEIN.
DR SMART: SM00977; WNT1.1.
DR PROSITE: PS00245; WNT1.1.
KW Developmental protein; Glycoprotein; Signal; Protein oncogene;
KW Extracellular matrix.
FT SIGNAL 1 23
FT CHAIN 22 352
FT CARBOHYD 70 70 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 355 AA: 49659 MW: F31CF65544E9C17 CRC64:

Query Match 41.4% Score 843.5 DB 1: Length 355:
Best Local Similarity 45.0% Pred. No. 2,4e+66:
Matches 156: Conservative 53: Mismatches 103: Indels 9: Gaps 3:

QY 31 KWSIVYASTNLTLDKSLQVLEPSDILSRKQRLIP--NTHHSVS3SDQSAVRECK 93

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Db 26 KWSLALGQYLTSLAS-----QPLTSSIPDLVAKLQFRCNVITIMNSVAEAKGLGIC 80
OY 94 KWQERNRNRNCPPTAPR-HLGKLVNCGEITFELTALTSAGVSHVANSQSGSTIES77 152
Db 81 QHQEGRNRNCTIDDSLAIFGPVLDKATRESAFVATLASAGVAFVATRSACAGSTIG 140
OY 153 CVYRRKQEP3PCDHWGQSDNIDFGRLEFGEFDSGEKQRLRPLMLHNNAGRTYES 212
Db 141 CDSHHKPRFGEKRWKQSGESDADFGVLYSEFEALAEENRPPAKAMKHNHNAAGTITLD 200
OY 213 EMROEPCGMSGSCVTRTCMKRLPTLRAGVYLRCFEDGASRVLYNKGNSNABAEILL 272
Db 201 HHMKCKCKGSLGSCSEVTKCMAQPDPRALIGFLKDKYDSASENVV---EKHRESQWVE 257
OY 273 RLEPEDAHKPPSPHLYVFEKSPNCTYSGRRLGAGTACRACNSSPALDG/ELLCCGR 332
Db 258 TLRAKVALFPRPTERLVLVYENSNPCEPNPEETGSGFRDTCVNTSHQIDGELLCCGR 317
OY 333 GHRTRTORVTERGNCITFMHCCHVSCRCNCTIRVLEEC 369
Db 318 GHNTRTEREKCKCHVFCVSCGECIRIDVHTC 354

RESULT 10
WNT4_XENLA
ID WNT4_XENLA STANDARD: PRT: 351 AA.
AC P49318: Q91927.
DT 01-FEB-1996 (rel. 33, Created)
DT 01-FEB-1996 (rel. 33, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE WNT-4 protein precursor (XMT-4).
GN WNT-4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9304810; PubMed=1425145;
RA McGrew L.L., Cline A.P., Moon R.T.;
RT "Analysis of Xmt-4 in embryos of Xenopus laevis: a Wnt family member
RT expressed in the brain and floor plate."
RL Development 115:463-473(1992).
RN [2]
RP SEQUENCE OF 261-351 FROM N.A.
RC TISSUE=Embryo;
RA MEDLINE=91122417; PubMed=1991549;
RA Christian J.L., Gavin B.J., McMahon A.F., Moon R.T.;
RT "Isolation of cDNAs partially encoding four Xenopus
RT Wnt-1/int-1-related proteins and characterization of their transient
RT expression during embryonic development."
RL Dev. Biol. 143:230-244(1991).
CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A
CC SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE
CC REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL
CC DIAMETERS.
CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE BRAIN AND FLOOR PLATE.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION DURING THE NEURULA THROUGH TAILFOLD
CC STAGES OF DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
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OY 6 LIPGWSATLLALALPALAANSSRWGVNVAASITNLTISKLVLEPSIQILS 65
Db 1 MTPYFLRSLMLLAVSANAAN-----WLYLAISSVGSISEHETKIKGP-----I 50
OY 66 KRORELLPONPILSHSVSGIUSAVRECKWQFRNRNMPCTAFGRHLE KLVNCGEITA 125
Db 51 QROVMKRNLELVMSVSRGAOLALIEQOYOFNRNRNMGSTLTLIIVPRKVOTGTREAA 110
OY 146 FFAITANVTHSVARSGESIESCTCYRRRGPGDPGPDHMKWNSR NTRGRLEFGREFF 185
Db 111 FVAVISAAVAVAVAVFANCSSELEKGCDDRTVHGSVPUGVGSQNSR NLTGVAFSISFV 170
OY 146 DSSEK--GQDLRELMNHNNEAGRTTVESEKQCKCHMSGS17V7VWRLPTLRAY 242
Db 171 LVPRKSGSSSRALMNLHNNEAGRAILNNNRKCKCHGVSSGLEVKCYKAMPTRKVV 230
OY 243 GNVKDFQASRVLYDNRGNSNABAEILLRLEPLFAHPRFCHLVYFEKSPNCTYES 312
Db 241 GNVKDFQASRVLYDNRGNSNABAEILLRLEPLFAHPRFCHLVYFEKSPNCTYES 312
OY 303 GRLGATATGACRACNSSPALDGCELLCCGKGRITQVTERKNITFMHCCHVSCRCNCTH 362
Db 284 LKNLVGLATITGRCQNKTSKALIDGCELMVGRGHTEVEIVERGSKRFRKQVTRKQJHR 343
OY 363 TRVLEEC 369
Db 344 VVEWHTC 450

RESULT 11
WNT3_HUMAN
ID WNT3_HUMAN STANDARD: PRT: 355 AA.
AC P56703: Q9H130.
DT 15-JUL-1999 (rel. 32, Created)
DT 15-JUL-2001 (rel. 40, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE WNT-3 proto-oncogene (protein precursor).
GN WNT3 OR INT4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Testa T.T., Mossakowska D.E., Carter P.S., Hu E., Zh. Y.,
RA Keisell D.P., Murdoch P.R., Heritty N.C., Lewis C.C., Boss D.A.,
RA Culbert A.A., Reith A.D., Barnes M.R.;
RT "Molecular cloning and characterization of six novel human Wnt
RT genes."

```

RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21490205; PubMed-11604997;  
 RA Katon M.;  
 RT "Molecular cloning and characterization of human WNT3";  
 RL Int. J. Oncol. 19:977-982(2001).  
 RN [3]  
 RP SEQUENCE OF 1-333 FROM N.A.  
 RX MEDLINE-94053935; PubMed-8244403;  
 RA Roelink H., Wang J., Black D.M., Solomon E., Nusse R.;  
 RT "Molecular cloning and chromosomal localization to 17q21 of the human WNT3 gene";  
 RL Genomics 17:790-792(1993).  
 CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN  
 CC TRANSMEMBRANE RECEPTORS. WNT-3 AND WNT-1A PLAY DISTINCT ROLES IN  
 CC CELL-CELL SIGNALING DURING M-PROGENESIS OF THE DEVELOPING NEURAL  
 CC TUBE (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the  
 CC extracellular matrix.  
 CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AY009397; AAC38657.1;  
 DR EMBL: AB067628; BAB70502.1;  
 DR Genew: HGNC:12782; WNT3.  
 DR MIM: 165330;  
 DR InterPro: IPR000970; Wnt\_glycylator.  
 DR Pfam: PF00110; wnt.1.  
 DR PRINTS: PR01349; WNTPROTEIN.  
 DR SMART: SM00097; WNT1.1.  
 DR PROSITE: PS00246; WNT1.1.  
 KW Developmental protein; Glycoprotein; Signal; Proto-oncogene;  
 KW Extracellular matrix;  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 355 WNT-3 PROTO-ONCOGENE PROTEIN.  
 FT CARBOHYD 90 90 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 301 301 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 355 AA; 39645 MW; 85D15F2C784A64F CRC64;  
 Query Match 41.38; Score 840.5; DB 1; Length 355;  
 Best Local Similarity 46.08; Pred. No. 4,4e-66;  
 Matches 155; Conservative 52; Mismatches 121; Indels 9; Gaps 3;

DB 318 GHTTETKREKCHXIFMHWVYSVECIETIVWHTO 354  
 RESULT 12  
 WNT4\_HUMAN STANDARD; PRT; 351 AA.  
 AC P56705; Q9HJ26; Q9HJ26; Q9HJ26;  
 DT 15-JUL-1999 (rel. 35, Created)  
 DT 15-JUN-2002 (rel. 41, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE WNT-4 protein precursor.  
 GN WNT4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Testa T.L., Messakoska L.E., Carter P.S., Hsiao E., Zhu Y.,  
 RA Kestell L.P., Murdoch P.R., Herity N.C., Lewis J.L., Cross J.A.,  
 RA Culbert A.A., Reith A.D., Barnes M.R.;  
 RT "Molecular cloning and characterization of six novel human WNT  
 RT genes";  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-2105589; PubMed-11283799;  
 RA Jordan B.K., Mohammed M., Ching S.T., Deiot E., Hsu X.N., Dowling P.,  
 RA Swain A., Rao P.N., Elejalde R.R., Vilain E.;  
 RT "Up-regulation of Wnt-4 signaling and dosage-sensitive sex reversal in  
 RT humans";  
 RL Am. J. Hum. Genet. 68:1102-1109(2001).  
 RN [3]  
 RP SEQUENCE OF 27-351 FROM N.A.  
 RA Pearce A.;  
 RT Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 210-329 FROM N.A.  
 RT TISSUE=Brain;  
 RX MEDLINE-94121588; PubMed-826086;  
 RA Hunter E.L., McMahon J.A., McMahon A.P., Hickin J., Harris A.L.;  
 RT "Differential expression of human Wnt genes 2, 3, 4, and 7b in human  
 RT breast cell lines and normal and disease states of human breast  
 RT tissue";  
 RL Cancer Res. 54:2615-2621(1994).  
 RN [5]  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RA Peltokeho H., Heikkila M., Vainio S.;  
 RT Submitted (Jan-2001) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RA Sim D.E., Smith A., Szallasi Z., Ioannou P., Lindsay M.H., Little M.H.;  
 RT "Expression of Wnt-4 but not 16 regulated by the Wnt3 tumor suppressor  
 RT gene, Wnt1";  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN  
 CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A  
 CC SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE  
 CC REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER AND BE ASSOCIATED WITH  
 CC ABNORMAL PROLIFERATION IN HUMAN BREAST TISSUE.  
 CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the  
 CC extracellular matrix.  
 CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.  
 CC -----  
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DR EMBL: AY009394: AAG365H.1:
DR EMBL: AF316543: AAK51692.1:
DR EMBL: AL031281: CAB52601.1:
DR EMBL: AF33591: AAK27651.1:
DR EMBL: AY033057: AAK50427.1:
DR GenBank: HGNC:12783: WNT4.
DR MIM: 603490:
DR InterPro: IPR000970: Wnt_glycdfactor.
DR Pfam: PF00110: wnt.1.
DR PRINTS: PR01349: WNTPROTEIN.
DR SMART: SM00097: WNT1.1.
DR PROSITE: PS00246: WNT1.1.
DR Developmental Protein: Glycoprotein: Signal.
KW SIGNAL.
FT CHAIN 1 22 WNT-4 PROTEIN.
FT CARBOHD 88 88 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHD 297 297 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 106 106 T->I (IN REF.1).
FT CONFLICT 111 111 F->L (IN REF.1).
SQ SEQUENCE 351 AA: 39051 MW: 46508755<9920AB CRO84:

Query Match 41.3% Score 840: DB 1: Length 351:
Best Local Similarity 44.8%: Pred. No. 4 se-6%:
Matches 161: Conservative 55: Mismatches 123: Indels 20: Gaps 4:

QY 14 TLTLALALPAALAASSGPMGIVNVAASNTLITKSLQVLEPSIDLSKQRLIR 73
DB 9 SIRLLVFAVSAASN-----WYLAKLSSVGSISEETICE-----KLKGLIRQVCK 58
QY 74 QNPGLHSVSGLSQAVRECKQKQFNRNRMWCPAPGPHLEFKIYNKCGRETAFITSA 133
DB 59 RILEVMDSVVRGAQLAIECCQYQFNRNRMWCTLSDLPFGKVVYTGIFEAFAVYALISA 118
QY 134 GVTSHVARSQSEGSIECTCYRRRGPGDPMHWGSCDNIIDRKFIFEFVDSKGR- 192
DB 119 GVAFAVTRACSSSELEKCCGDRIVHVSFGQFGWSJLSNLAIVAAVSQSPVVRERSKG 178
QY 193 --DLFLMNLHNEAGRTVSEMKQCKCHGMSGCTVTRCKMRLTLAAVDVLRDF 250
DB 179 ASSSRAALMNLHNEAGRTVSEMKQCKCHGMSGCTVTRCKMRLTLAAVDVLRDF 238
QY 251 DGASRVLYNRGNSRASRAELLEPEDPAPHKPSPHDLVYFEKSPFCTYSRLTAGT 310
DB 239 DQATEVEPRKVGSSRA-----LVPRNAQFPRHTDELDVLEPSDFECQDMRSVLGT 291
QY 311 AGACNSSPALDGCCLCGRGHRTQVTRCKMCTHMCCHVSCNCTHRYVHEG 369
DB 292 RRTCKNTSKAIDGCELLCGCGRHQAQVELAERCGCFHMCQCFKQCQCLVELHTO 350

RESULT 13
WNT4_MOUSE STANDARD: PRT: 351 AA.
AC P22724:
DT 01-AUG-1991 (Rel. 19: Created)
DT 01-AUG-1991 (Rel. 19: Last sequence update)
DT 15-JUN-2002 (Rel. 41: Last annotation update)
DE WNT-4 protein precursor.
GN WNT4 OR WNT-4.
OS Mus musculus (Mouse).
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
OX NCBI_TaxID=10090:
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91122614: PubMed-2279700:
RA Gavin B.J., McMahon J.A., McMahon A.P.:
RT Expression of multiple novel wnt-1/int-1-related genes during fetal
RT and adult mouse development.
RC Genes Dev. 4:2319-2332(1990).
CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS. MAY BE AN INTRACELLULAR SIGNALING
CC MOLECULE INVOLVED IN SEGMENTATION OF THE FOREBRAIN. IS LIKELY TO

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CC SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SMITH ET AL.). SEEMS TO BE
CC INVOLVED IN KIDNEY DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -!- TISSUE SPECIFICITY: IN ADULTS IN LUNG AND BRAIN.
CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: M89797: AAA10564.1:
DR PIR: G36470: G36470.
DR MIM: MGI:98957: Wnt4.
DR InterPro: IPR000970: Wnt_glycdfactor.
DR Pfam: PF00110: wnt.1.
DR PRINTS: PR01349: WNTPROTEIN.
DR SMART: SM00097: WNT1.1.
DR PROSITE: PS00246: WNT1.1.
KW Developmental Protein: Glycoprotein: Signal.
FT SIGNAL 1 22 WNT-4 PROTEIN.
FT CHAIN 23 351 WNT-4 PROTEIN.
FT CARBOHD 88 88 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHD 297 297 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 351 AA: 39049 MW: 7610507398593909 CRO84:

Query Match 41.1% Score 836: DB 1: Length 351:
Best Local Similarity 44.6%: Pred. No. 1 se-6%:
Matches 160: Conservative 55: Mismatches 124: Indels 20: Gaps 4:

QY 14 TLTLALALPAALAASSGPMGIVNVAASNTLITKSLQVLEPSIDLSKQRLIR 73
DB 9 SIRLLVFAVSAASN-----WYLAKLSSVGSISEETICE-----KLKGLIRQVCK 58
QY 74 QNPGLHSVSGLSQAVRECKQKQFNRNRMWCPAPGPHLEFKIYNKCGRETAFITSA 133
DB 59 RILEVMDSVVRGAQLAIECCQYQFNRNRMWCTLSDLPFGKVVYTGIFEAFAVYALISA 118
QY 134 GVTSHVARSQSEGSIECTCYRRRGPGDPMHWGSCDNIIDRKFIFEFVDSKGR- 192
DB 119 GVAFAVTRACSSSELEKCCGDRIVHVSFGQFGWSJLSNLAIVAAVSQSPVVRERSKG 178
QY 193 --DLFLMNLHNEAGRTVSEMKQCKCHGMSGCTVTRCKMRLTLAAVDVLRDF 250
DB 179 ASSSRAALMNLHNEAGRTVSEMKQCKCHGMSGCTVTRCKMRLTLAAVDVLRDF 238
QY 251 DGASRVLYNRGNSRASRAELLEPEDPAPHKPSPHDLVYFEKSPFCTYSRLTAGT 310
DB 239 DQATEVEPRKVGSSRA-----LVPRNAQFPRHTDELDVLEPSDFECQDMRSVLGT 291
QY 311 AGACNSSPALDGCCLCGRGHRTQVTRCKMCTHMCCHVSCNCTHRYVHEG 369
DB 292 RRTCKNTSKAIDGCELLCGCGRHQAQVELAERCGCFHMCQCFKQCQCLVELHTO 350

RESULT 14
WNT4_RAT STANDARD: PRT: 351 AA.
AC Q9XQ05:
DT 16-OCT-2001 (Rel. 40: Created)
DT 16-OCT-2001 (Rel. 40: Last sequence update)
DT 15-JUN-2002 (Rel. 41: Last annotation update)
DE WNT-4 protein precursor.
GN WNT4 OR WNT-4.
OS Rattus norvegicus (Rat).
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus
OX NCBI_TaxID=10116:
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE-Corpus luteum;
RA Lacher M.D., Walther P.R., Lareu R., Dharmarajan A.M., Frits R.F.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS. MAY BE AN INTRACELLULAR SIGNALING
CC MOLECULE INVOLVED IN SEGMENTATION OF THE FOREBRAIN. IS LIKELY TO
CC SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sdb.ch).
CC
CC EMBL: AF186608; AAF15589.1;
CC InterPro: IPR000970; Wnt_gntfactor.
CC Pfam: PF00110; Wnt1.1.
CC SMART: SM00097; WNT1.1.
CC PROSITE: PS00245; WNT1.1.
CC Developmental protein; Glycoprotein; Signal.
CC SIGNAL 1 22 POTENTIAL.
CC FT CHAIN 23 351 WNT-4 PROTEIN.
CC FT CARBOHYD 84 88 N-LINKED (GLCNAc...) (POTENTIAL).
CC FT CARBOHYD 257 297 N-LINKED (GLCNAc...) (POTENTIAL).
CC SEQUENCE 351 AA: 39043 MW: 59080.334502BAI CRC04;

Query Match 41.1% Score 836; DB 1; Length 351;
Best Local Similarity 44.6% Pred. No. 11e-65;
Matches 160; Conservative 55; Mismatches 124; Indels 20; Gaps 4;

OY 14 TLTLALALPAALAASSGRMMGIYVASSINILTSKSLQVLEPSSLOLSKRPQLIR 73
DB 9 SRLILYAVFVSAASN-----WLYLAKSSVSSISEETCE-----KLKGLIRQVGMK 58
OY 74 QNRGILHSVSGLSAVRECKQKQFNRKRNPTAPRPHLFGKIVNKGCFATATPATA 133
DB 59 RNLEVKOSVRHQAQLALEQDQFNRKRNKSTLLPLFGKIVNKGCFATATPATAVATSSA 118
OY 134 GYTHSVARSCEGSIESTCTDYPRRPGGPDMMHWSQSDNIIEGRLEFGRFVDSSEKRP 192
DB 119 GVAFAVTAACSSGLEKGGCDRTVAGVSPQFQMSQSDNIAYGVAFGQSPFVREKSKG 178
OY 193 --DLPFLNLIHNNAGRTTFSEMRQECCKHMSGSCSTVPTNMLPTLAVGDLVRESE 250
DB 179 ASSRPAIANKLNHNNAGRKAILTHKRVKCKHGVSSGKVKTWRAVAPPPQVHAKREK 248
OY 251 DGASRVLYGNFGRNRSRAELRLLEDPAPAKPPSPHLVYERKSPNCTYSPLSLTAIT 310
DB 239 DQATEVEPRRVGSSRA-----LVPRNAQPKRPHDDELYLESPDCEQDMKSGYLDT 291
OY 311 AGACNSSSPALDCCGCGGRTPTQPTERKCTPHMGCCHSCNCHRVLAIEG 369
DB 292 RQHTCNKTSKAIIDSCGELGCGRGPHITAHVLAELKMGCGPRHMCVKNHQCQRLVEMHT 350

RESULT 15
WNT4_CHICK STANDARD: PRF: 351 AA.
AC P49337;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE WNT-4 protein precursor.
OS Gallus gallus (chicken).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

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OC Gallus.
OX NCBI_TaxId=9031;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE-Embryo;
RL MEDLINE=6012034; PubMed=7948308;
RX Yoshida K., Ohuchi H., Nohno T., Fujiwara A., Tada N.,
RA Kawakami Y., Noji S.;
RT "Regional expression of the Wnt-4 gene in developing chick central
RT nervous system in relationship to the diencephalic neuromere D2 and a
RT dorsal domain of the spinal cord";
RL Biochem. Biophys. Res. Commun. 203:1581-1588(1994).
RN 12
RP SEQUENCE FROM N.A.
RL MEDLINE=6063018; PubMed=7574541;
RX Tada N., Kawakami Y., Saito T., Noji S., Nohno T.;
RT "Cloning and characterization of Wnt-4 and Wnt-11 cDNAs from chick
RT embryo.";
RL DNA Seq. 5:277-281(1995).
CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS. MAY BE AN INTRACELLULAR SIGNALING
CC MOLECULE INVOLVED IN SEGMENTATION OF THE FOREBRAIN INTO THE
CC NEUROMERE D2 AND IN DIFFERENTIATION OF THE DORSAL REGION OF THE
CC SPINAL CORD. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE DENCEPHALON
CC NEUROMERE D2.
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC
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CC or send an email to license@sdb-sdb.ch).
CC
CC EMBL: D01600; BA066948.1;
CC InterPro: IPR000970; Wnt_gntfactor.
CC Pfam: PF00110; Wnt1.1.
CC SMART: SM00097; WNT1.1.
CC PROSITE: PS00245; WNT1.1.
CC Developmental protein; Glycoprotein; Signal.
CC SIGNAL 1 22 POTENTIAL.
CC FT CHAIN 23 351 WNT-4 PROTEIN.
CC FT CARBOHYD 84 88 N-LINKED (GLCNAc...) (POTENTIAL).
CC FT CARBOHYD 257 297 N-LINKED (GLCNAc...) (POTENTIAL).
CC SEQUENCE 351 AA: 39043 MW: 59206.929446A6I CRC04;

Query Match 40.5% Score 822; DB 1; Length 351;
Best Local Similarity 42.7% Pred. No. 2.4e-65;
Matches 156; Conservative 55; Mismatches 124; Indels 20; Gaps 4;

OY 8 FQWVAITLLALPAALAASSGRMMGIYVASSINILTSKSLQVLEPSSLOLSKRP 67
DB 3 FENILPPELLILATPSAASN-----WLYLAKSSVSSISEETCE-----KLKGLIOR 52
OY 68 QRLILQNPGLIHSVSGLSAVRECKQKQFNRKRNPTAPRPHLFGKIVNKGCFATFI 127
DB 53 QVQMKRNELEVKOSVRHQAQLALEQDQFNRKRNKSTLLPLFGKIVNKGCFATFI 112
OY 128 FAITSVATHSVARSCEGSIESTCTDYPRRPGGPDMMHWSQSDNIIEGRLEFGRFVDS 187
DB 113 VAISASVAVTAACSSGLEKGGCDRTVAGVSPQFQMSQSDNIAYGVAFGQSPFVREK 172
OY 188 GKRQRL --RPLNLIHNNAGRTTFSEMRQECCKHMSGSCSTVPTNMLPTLAVGDLV 244
DB 173 BRKSGASNRKALNHNAGRKAILNHNAGRKAILNHNAGRKAILNHNAGRKAILNHNAG 232
OY 245 V--RDFPDASRVLYGNFGRNRSRAELRLLEDPAPAKPPSPHLVYERKSPNCTYSR 304

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Db 233 VLKRFQATBEVSELSISKY-----LVFKNSQFKPHIDEVLVLDSSPDICT 95  
QY 305 LSTAGTAGACNSSSPALDGCCELLCGRGHRTPTQKVTETRCNTEPHWCHVSCNCTH 344  
Db 286 NGVLTSTSRQCNKTSKALDGCCELLMCGRGPHIDEVEVEVKCSCKFHWCCSVKCKE HRYT 345  
QY 365 VLHEC 369  
Db 346 EIHIC 350

Search completed: April 22, 2003, 16:39:47  
Job time : 26 secs

GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2003, 16:36:48 ; Search time 87 Seconds  
(without alignments)  
876.292 Million cell updates/sec

Title: US-09-674-292-1

Perfect score: 2036  
Sequence: 1 MOLMALLPGWASATILLALA.....WCHVSGRNCITHTPYLHCL 370

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_21:\*

1: sp.archaea:\*

2: sp.bacteria:\*

3: sp.fungi:\*

4: sp.human:\*

5: sp.invertebrate:\*

6: sp.mammal:\*

7: sp.mhc:\*

8: sp.organelle:\*

9: sp.phage:\*

10: sp.plant:\*

11: sp.podent:\*

12: sp.virus:\*

13: sp.vertebrate:\*

14: sp.unclassified:\*

15: sp.virus:\*

16: sp.bacteriap:\*

17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1598	78.5	370	13	P79752 fugu rubrip
2	1203.5	59.1	262	13	O96779 oryzias lat
3	1151	55.5	394	5	O96866 gryllus him
4	1127.5	55.4	374	5	O81396 cupieninus
5	1064.5	52.3	377	5	O61699 bianchiosto
6	878.5	43.1	365	5	O8W877 mysidium co
7	866.5	42.6	303	5	O9T864 tribolium c
8	834	41.0	353	5	O9T776
9	818	40.2	376	13	O9PWH1
10	800.5	39.3	395	5	O8W876
11	785	38.5	360	11	O9CZW3
12	783	38.5	358	13	O9IAU3
13	779	38.0	350	13	O8W839
14	774.5	38.0	365	13	O985N7
15	768.5	37.7	380	11	O8VCV6
16	767	37.7	250	5	O27671

Result No.	Score	Query Match	Length	DB ID	Description
17	765.5	37.6	370	5	O6W875
18	765.5	37.6	385	13	O968X6
19	765	37.6	311	11	O968X5
20	764	37.5	315	13	O968X4
21	753	37.3	267	13	O8W817
22	754	37.1	381	5	O8T395
23	749	36.8	372	11	O91XPS
24	748.5	36.8	371	5	O8T8A8
25	747.5	36.7	331	5	O86867
26	741.5	35.4	384	13	P79856
27	737	35.2	360	5	O904V0
28	724.5	35.6	349	13	O42258
29	720.5	35.4	343	4	O968H0
30	720.5	35.4	344	11	O968Y3
31	709.5	34.8	347	5	O61700
32	707.5	34.7	349	13	O96F88
33	694.5	33.5	390	13	P79753
34	678.5	33.5	348	13	O13266
35	678.5	33.5	348	13	O13266
36	672.5	33.0	351	5	O96NC0
37	671	33.0	351	5	O96W74
38	670.5	32.7	452	5	P91051
39	667	32.7	443	5	O963J9
40	650	32.2	315	11	O92058
41	650	32.2	315	11	O91V55
42	646.5	31.4	352	13	O91912
43	646	31.4	363	11	O858M2
44	642.5	31.5	359	11	O8V190
45	640.5	31.5	293	4	O91P30

## ALIGNMENTS

RESULT 1

ID P79752 PRELIMINARY: PRT: 370 AA.

AC P79752:

DT 01-MAY-1997 (TEMBLrel: 03, Created)

DT 01-MAY-1997 (TEMBLrel: 03, Last sequence update)

DT 01-JUN-2002 (TEMBLrel: 21, Last annotation update)

DE Wnt1.

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Acanthopterygii; Perciformes; Tetraodontidae; Takifugu.

OX NCBI\_TaxID:81033

FN [1]

FP SEQUENCE FROM N.A.

RX MEDLINE=9177347; PubMed=10075341

RA Gellner K., Brenner S.

RI "Analysis of 148 kb of genomic DNA around the wnt1 locus of Fugu rubripes."

RL Genome Res. 9:251-256(1997).

CC -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.

DR EMBL: AF056116; AAC34388.1; ..

DR InterPro: IPR000970; Wnt\_anti-factor.

DR Pfam: PF00110; Wnt\_1.

DR PRINTS: PF01349; WNTPROTEIN.

DR SMART: SM00097; WNT1.1.

DR PROSITE: PS00246; WNT1.1.

KW Developmental protein; Glycoprotein.

SQ SEQUENCE 370 AA: 41950 MW: 180018565CEFEK...C...C...

Query Match 78.5% Score 1598; Len 370; Length 370;

Best Local Similarity 78.5%; Pred No. 86-116;

Matches 262; Conservative 41; Mismatches 43; Gaps 2;

QY ALPGWASATILLALPAALPAALANSGRKMGIVNASTNLTITSSGLVTPESLDT 64

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Db 5 ALLG-VKACILLVSSLTGTGAVNNSSRMWGIYVASSNLTITSKVQVLDPISALL 63
QY 65 SRKORLLRQNPGLHSVSGJQSQAVRECKQKQFNNRPNCPAPRPHLPGKIVNRGCRET 124
Db 64 SRKORLLRQNPGLHSVSGJQSQAVRECKQKQFNNRPNCPAPRPHLPGKIVNRGCRET 123
QY 125 APTFAITASVTHSVASCSSEGSIESCTGDFRRFGDPGMWAGCSNITFEGELGEPFE 184
Db 124 APTFAITASVTHSVASCSSEGSIESCTGDFRRFGDPGMWAGCSNITFEGELGEPFE 183
QY 185 VDSGKGLRFLMLNHNPAQTIVFSEMRQCKTHNSGCTVTRTCWMLPTLAVGD 244
Db 184 VDSGKGLRFLMLNHNPAQTIVFSEMRQCKTHNSGCTVTRTCWMLPTLAVGD 243
QY 245 VLRFEDGASRVLYGNHNSNRS-RAELLRLPEPDPAHPPSPHDLVFEKSPNCTYSG 303
Db 244 FLKDFDGASRVYANKGNSRASHAHRLPEPDPAHPPSPHDLVFEKSPNCTYSG 303
QY 304 RLGTATGTRACNSSPALDGCGLCCGGRHRTGQVIERGNCITFHHCHVSTRNTH 363
Db 304 KICITLGTGRACNSTPGDGCGLCCGGRHRTGQVIERGNCITFHHCHVSTRNTH 363
Db 364 RLHCECL 370
Db 364 RLHCEV 370

RESULT 2
QYPT79 PRELIMINARY: PRT: 262 AA.
AC QYPT79:
DT 01-MAY-2000 (TEMBREL: 13, Created)
DT 01-MAY-2000 (TEMBREL: 13, Last sequence update)
DT 01-JUN-2002 (TEMBREL: 21, Last annotation update)
DE Wnt-1 (Fragment).
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Blotiliformes; Atherinichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP Carl M. Witbrodt J.:
RA "Graded interference with FGF-signalling uncovers its dorso-ventral
RT asymmetry at the mid-hindbrain boundary."
RL Submitted (JUN-1999) to the EMBL/GenBank/Tran databases.
DR EMBL: AJ243208; CAB64448.1;
InterPro: IPR001230; Pfam: Pfam_1;
InterPro: IPR000970; Wnt_gtfhactor.
PR PRT: PF00110; wnt: 1.
PS PRINTS: PR01349; WNTPROTEIN.
DR SMART: SM00097; WNT1: 1.
DR PROSITE: PS00294; PRENYLATION; UNKN.WN.1.
FT NON_TER 1
FT TER 262
FT NON_TER 1
SQ SEQUENCE 262 AA; 29267 MW; 5563A1660A5E5F03; RC04;

Query Match 59.1%; Score 120.5; Db 1%; Length 262;
Best Local Similarity 79.8%; Pred. No. 6,2e-108;
Matches 209; Conservative 21; Mismatches 29; Indels 1; Gaps 1;
QY 96 OFNRFRNCPAPRPHLPGKIVNRGCRETAPRPHLPGKIVNRGCRETAPRPHLPGKIVNRGCRET 155
Db 1 OFNRFRNCPAPRPHLPGKIVNRGCRETAPRPHLPGKIVNRGCRETAPRPHLPGKIVNRGCRET 60
QY 156 RRRGPGDPGMWAGCSNITFEGELGEPFEVNSGKGLRFLMLNHNPAQTIVFSEMR 215
Db 61 RRRGPGDPGMWAGCSNITFEGELGEPFEVNSGKGLRFLMLNHNPAQTIVFSEMR 120
QY 216 QECCHGSSCTVTRTCWMLPTLAVGDVLRFEDGASRVLYGNHNSNRS-RAELLPL 274
Db 216 QECCHGSSCTVTRTCWMLPTLAVGDVLRFEDGASRVLYGNHNSNRS-RAELLPL 274

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Db 121 QECCHGSSCTVTRTCWMLPTLAVGDVLRFEDGASRVLYGNHNSNRS-RAELLPL 180
QY 275 EPEDPAHPPSPHDLVFEKSPNCTYSGLTATGACANSSNPAIDGCELLCGGRH 334
Db 181 EPEDPAHPPSPHDLVFEKSPNCTYSGLTATGACANSSNPAIDGCELLCGGRH 240
QY 335 PRTQVTRGNCITFHHCHVSTRNTH 366
Db 241 KTRSAVTRGNCITFHHCHVSTRNTH 262

RESULT 3
QYGRAG6 PRELIMINARY: PRT: 394 AA.
AC QYGRAG6:
DT 01-MAR-2001 (TEMBREL: 16, Created)
DT 01-MAR-2001 (TEMBREL: 16, Last sequence update)
DT 01-JUN-2002 (TEMBREL: 21, Last annotation update)
DE Wingless protein.
OS Oryzias latipes (Two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensiteria; Gryllidae;
OC Gryllinae; Gryllus.
OX NCBI_TaxID=6959;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461145; PubMed=11003837;
RA Nika N., Inoue Y., Nozawa A., Saito M., Misumi Y., Inoue H.,
RA Yoshitaka H., Noji S.:
RT "Correlation of diversity of leg morphology in Oryzias latipes
RT (cricket) with divergence in dpp expression pattern during leg
RT development."
RL Development 127:4373-4381(2000).
DR EMBL: AB044713; BAB16640.1;
DR InterPro: IPR000345; Cytochrome_b;
DR InterPro: IPR000970; Wnt_gtfhactor.
PR PRT: PF00110; wnt: 1.
PS PRINTS: PR01349; WNTPROTEIN.
DR SMART: SM00097; WNT1: 1.
DR PROSITE: PS00294; CYTOCHROME; UNKN.WN.1.
DR PROSITE: PS00245; WNT1: 1.
SQ SEQUENCE 394 AA; 43650 MW; CA2FEFID50DDAA; RC 14;

Query Match 56.5%; Score 1151; Db 5%; Length 394;
Best Local Similarity 57.0%; Pred. No. 1.2e-102;
Matches 219; Conservative 45; Mismatches 90; Indels 39; Gaps 0;
QY 15 LILALALPALALAN---SSGF---WMIYVASSNLTITDSKSLQVLEPSTQ-LLSRK 67
Db 11 LILALALPALALAN---SSGF---WMIYVASSNLTITDSKSLQVLEPSTQ-LLSRK 69
QY 68 QRLTFQNPGLHSVSGJQSQAVRECKQKQFNNRPNCPAPRPHLPGKIVNRGCRET 124
Db 70 QRLTFQNPGLHSVSGJQSQAVRECKQKQFNNRPNCPAPRPHLPGKIVNRGCRET 125
QY 125 APTFAITASVTHSVASCSSEGSIESCTGDFRRFGDPGMWAGCSNITFEGELGEPFE 184
Db 125 APTFAITASVTHSVASCSSEGSIESCTGDFRRFGDPGMWAGCSNITFEGELGEPFE 183
QY 185 VDSGKGLRFLMLNHNPAQTIVFSEMRQCKTHNSGCTVTRTCWMLPTLAVGD 244
Db 185 VDSGKGLRFLMLNHNPAQTIVFSEMRQCKTHNSGCTVTRTCWMLPTLAVGD 243
QY 245 VLRFEDGASRVLYGNHNSNRS-RAELLRLPEPDPAHPPSPHDLVFEKSPNCTYSG 303
Db 245 VLRFEDGASRVLYGNHNSNRS-RAELLRLPEPDPAHPPSPHDLVFEKSPNCTYSG 303
QY 304 RLGTATGTRACNSSPALDGCGLCCGGRHRTGQVIERGNCITFHHCHVSTRNTH 363
Db 304 RLGTATGTRACNSSPALDGCGLCCGGRHRTGQVIERGNCITFHHCHVSTRNTH 363
QY 364 RLHCECL 370
Db 364 RLHCEV 370

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DB 370 HCTFHMCEVCKCTCHVAKTIHTC 393

## RESULT 4

Q87396 PRELIMINARY: PRT: 374 AA.

AC Q87396: 01-JUN-2002 (TREMblrel: 21, Created)

DT 01-JUN-2002 (TREMblrel: 21, Last sequence update)

DT 01-JUN-2002 (TREMblrel: 21, Last annotation update)

DE Wingless.

GN Wg.

OS Cupiemus salet (Wandering spider).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;

OC Araneomorphae; Entelelynae; Lycosidae; Ctenidae; Cupiemus.

OX NCBI\_TaxID=6928;

3N [1]

4P SEQUENCE FROM N.A.

RX MEDLINE=216363; PubMed=11874919;

RA Damen W.G.M.;

RT "Parasemental organization of the spider embryo implies that the parasemental is an evolutionary conserved entity in arthropod

RT embryogenesis";

RL Development 129:1235-1250(2002).

DR EMBL: AJ15945; CAC87040.1; -

SQ SEQUENCE 374 AA: 42220 MW: 0F60F0F10D94C400 CRC64:

Query Match 55.4%: Score 1127.5; DB 5; Length 374;

Best Local Similarity 56.2%: Pred. No. 2.1e-100;

Matches 204; Conservative 51; Mismatches 97; Indels 11; Gaps 6;

QY 14 TLLALALPALAANSSGRWGVVNVASTNLTDKSLQVLE--PSLOC-LSRQGR 70  
 DB 17 TLLPAQAKPRHRGQGRG--RWSLSLASEPTLVLDVDRHGRGSKMDGPAHLPLKKQGR 75  
 QY 71 LTRONPILHSVSGLOSAYVECKWQFRNRRWNCPTAP---GRLFGKLVNHCPTAFI 127  
 DB 76 LVKNDPAMQALGRGVKVAISECKYQFKRRPNCPTADHARGNKINFGKIYQCGHEPAFL 135  
 QY 128 FAITSATVTHSVARSCSGESTGCDYRRGRGPGDMHWSGSDNIDGRPLGSPHYVDS 167  
 DB 136 YAITSAVTHSLSRACREGLVSTNCIDYRRGPSLIRHEWGGSDNIDGAAFSNGYDA 155  
 QY 188 GEGKGRDLFLMLNLHNNAGRTVYSEKROECKCHGSGSCTVPTQWRLPTLRAGGVYLR 247  
 DB 196 SERGKDLRYIMNLHNNENAGRAHYIGMRQCKCHGSGSCTVPTQWMLSPFRITIGDLK 255  
 QY 248 DRFGASRVLYGNRGSNRSAPALLRLLEPEDPAHKPPSPHLYVEFKSPNPTYSGRIGT 307  
 DB 256 DRFGASRVLYGNRGR--RRALK--PYHPEHKPPSKKLIVFENSDFPCYADPSLGH 311  
 QY 308 AGTAGRACNSSPALDGCGLCGRGHRTIQRVTERNCNCTFHMCCHVGRNGCTRYLH 367  
 DB 312 SATIGRTCNSSSLGVGCDLCCGGRGKSENNREYVRCNCTFHMCQVECKTKTKPLVH 371  
 QY 368 ECL 370  
 DB 372 ECL 374

## RESULT 5

Q61699 PRELIMINARY: PRT: 477 AA.

AC Q61699: 01-AUG-1998 (TREMblrel: 07, Created)

DT 01-JAN-1999 (TREMblrel: 09, Last sequence update)

DT 01-JUN-2002 (TREMblrel: 21, Last annotation update)

DE Amphibmtl.

GN WNT1

OS Branchiostoma floridae (Florida lancelet) (Amphioxus).

OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

OC Branchiostoma.

OX NCBI\_TaxID=7739;

3N [1]

4P SEQUENCE FROM N.A.

RX MEDLINE=20544609; PubMed=1110906;

RA Schubert M., Holland L.Z., Holland N.D., Jacobs J.K.

RT "A Phylogenetic Tree of the Wnt Genes Based on All Available Full-

RT Length Sequences, Including Five from the Cephalochordate Amphioxus";

RL Mol. Biol. Evol. 17:1896-1906(2000);

CC - FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).

CC - SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE

CC EXTRACELLULAR MATRIX (BY SIMILARITY).

CC - SIMILARITY: BELONGS TO THE WNT FAMILY.

DR EMBL: AF01594; AAC0432.1; -

DR InterPro: IPR000970; Wnt\_determinator.

DR Pfam: PF01133; Wnt.....

DR PRINTS: PR01449; WNTPROTEIN.

DR SMART: SM00474; WNT1.1.

DR PROSITE: PS00446; WNT1.1.

DR Developmental protein: Glycogen-protein.

SQ SEQUENCE 377 AA: 42451 MW: EFA56F1C7F9E9E9B 30044;

Query Match 52.9%: Score 1064.5; DB 5; Length 377;

Best Local Similarity 51.1%: Pred. No. 2.5e-94;

Matches 191; Conservative 64; Mismatches 102; Indels 21; Gaps 6;

QY 13 ATLLALALPALAANSSGRWGVVNVASTNL--LTSKSLQVLEPSLOLISF 66  
 DB 9 AVLLFLAVPVERVHNVIGRMWGLASTVAAGERANVPVAAKPSITIMLDPKRIPLNK 68  
 QY 67 KQRLKTRONPGLILSVSGLOS-----AVPECKWQFRNRRWNCPTAP---LFGKIV 117  
 DB 69 KQRLKTRONPGLILSVSGLOS-----LACHEEDPREMLAIKECHQSKWKNRIVNISDVANSVFNIL 123  
 QY 118 NRGCEPTAFTHSASVTHSVARSCSGESTGCDYRRGRGPGDMHWSGSDNIDGRPLGSPHYVDS 177  
 DB 124 LRSTLTAFIYAVSAVAHVEGRNCABGTLPTCSQYRRKGRHFEWEGSDNIDGR 183  
 QY 178 MLEPPEYVSGKGRDLFLMLNLHNNAGRTVYSEKROECKCHGSGSCTVPTQWRLPTLRAGGVYLR 246  
 DB 184 KQFAKFLVAGKPKIKVYPTLVNHNENAGRAVAENLPLETKYHMSSTLTKTWMPFL 243  
 QY 227 PTLRAGGVYLRLEPDLGASRVLYGNRGSNRSAPALLRLLEPEDPAHKPPSPHLYVEFKSP 295  
 DB 244 INFRHIGNSLKKRFLGASRVLYGNRGSNRSAPALLRLLEPEDPAHKPPSPHLYVEFKSP 303  
 QY 297 NCTYSGRGLTAGTAGRACNSSPALDGCGLCGRGHRTIQRVTERNCNCTFHMCCHVGRNGCTRYLH 356  
 DB 304 NCTYSGRGLTAGTAGRACNSSPALDGCGLCGRGHRTIQRVTERNCNCTFHMCCHVGRNGCTRYLH 363  
 QY 357 GRNCTHIVLECL 370  
 DB 364 CEETVYTKTIHTCL 377

## RESULT 6

Q8WPF7 PRELIMINARY: PRT: 365 AA.

AC Q8WPF7: 01-MAR-2002 (TREMblrel: 20, Created)

DT 01-MAR-2002 (TREMblrel: 20, Last sequence update)

DT 01-JUN-2002 (TREMblrel: 21, Last annotation update)

DE Signaling protein: Wingless (Fragment).

GN Wg.

OS Drosophila melanogaster.

OC Eukaryota; Metazoa; Arthropoda; Insecta; Malacostraca;

OC Eukaryota; Metazoa; Arthropoda; Insecta; Malacostraca; Diptera; Muscidae;

OX NCBI\_TaxID=10455;

3N [1]

4P SEQUENCE FROM N.A.

RA Duran Schaub M., Fink N., Patel N.B.;

RT "Analysis of the expression pattern of Wnt signaling in the wingless

RT protein: evidence for conserved mesodermal and ventral patterning

RT proteins: Wnt1, Wnt2, and Wnt3a in Drosophila wingless";



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RL Submitted (OCT-2001) to the EMBL/GenBank/EBI databases.
DR EMBL: AF438265; AAL37756.1; Wnt_grbthfactor.
DR InterPro: IPR000970; Wnt_grbthfactor.
DR Pfam: PF00110; Wnt1.
DR PRINTS: PR01349; WNTPROTEIN.
DR SMART: SM00097; WNT1.1.
DR PROSITE: PS00246; WNT1; UNKNOW_N.
FT NON_TER 365
SQ SEQUENCE 365 AA: 45624P911336A01 (RC64);

Query Match: 43.1%; Score 878.5; DB 5; Length 365;
Best Local Similarity 45.9%; Pred. No. 2,2e-75;
Matches 169; Conservative 62; Mismatches 106; Indels 31; Gaps 6;

OY 7 LFGWVSATLLALALPAALANSSGR-----WMTIVVASTNL-----LIDSKSLQ 95
D 1 MPAPGAAVFL-IALALAFVCEAQAQRYGPKWMLLSVTPSLMSNLTLSLSLDR 59
D 56 VLEPSLOTLNRKQRPFLPGNPGLHSVSGLSQSAVEYKWFPPNPNKCTA-----PSP 110
D 60 LSESYGRMLRKKQRLIRENCGVLAIAEAKKAASVYCFRFRDRDCASAKKTKR 119
D 111 HLFKYNKQRETAFITFAGYTHSVARSSEVSEIESTCIYRRKGQGVUHWGQC 170
D 120 RLFGHIVSIPCFETAFVALLSAVLSHVRACTEGAVHSCVHYTK--GDDWEMGQC 176
OY 171 SENIDFGRLGREFVDGSGKGRDPLMNLNHNEACRTTVESEKROCKCHGSGSCYR 230
D 177 SENIDFGYRSHFVDAGKEITHEIRAMNLHNEAPROVIVRAARSECKCHGSGCYR 236
OY 231 TGMWRLPLRAVDVLRDFGASVFL-----YGNRGSNRASRALLRELEDP 279
D 237 TGMWRLPLRQKIDRLKEKFDGASVSRHTAHMGRSRSRSTKRRFRKRLDLPYP 296
OY 280 AHRPPSPHDLVEYKSPNCTYSRLGTAAGRAVNSPALDCCCLCCGGRHTRTQ 339
D 297 DKKSSAAMDLYLQESPNCVNRRTIGPISERECNGTSISVDCNLMCCGGRYSRV 356
OY 340 RYTERKNC 347
D 357 EVERKSC 364

RESULT 7
OY1X64 PRELIMINARY: PRT; 303 AA.
AC OY1X64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Wingless product (Fragment).
Tribolium castaneum (Red flour beetle).
Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Tenebrionidae; Tribolium.
OX NCBI_TaxID=7070;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=94150623; PubMed=8107804;
RA Nagy L.M., Carroll S.;
RT "Conservation of wingless patterning functions in the short-germ
embryos of Tribolium castaneum.";
RL Nature 367:460-463(1994).
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
EXTRACELLULAR MATRIX (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
CC InterPro: IPR000970; Wnt_grbthfactor.
DR Pfam: PF00110; Wnt1.1.
DR SMART: SM00097; WNT1.1.
DR PROSITE: PS00246; WNT1.1.
KW Developmental protein; Glycoprotein.
FT NON_TER 1

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FT NON_TER 343
SQ SEQUENCE 365 AA: 34028 MW: E2B367B06A5984; 74.41;

Query Match: 42.6%; Score 866.5; DB 5; Length 365;
Best Local Similarity 53.5%; Pred. No. 2.5e-75;
Matches 162; Conservative 39; Mismatches 51; Indels 41; Gaps 6;

OY 109 GHLEKRYVNGRETFEATISAGYTHSVARSSEIESTCTCTCTPPEP-----RPGS 162
D 1 GNLFGKIVLKQGRERAFYATISAAVTAHIAACSESDITCNTRHKKRHHNSGNS 60
D 163 -----FDMHWGCGSNIDFRLGHRFVDGSGKGRDRLFMNLHNEAKITVESEKQ 216
D 41 GALAGVDFEFGGCGSDNIGFQTVSRFVDAGRGKTTREKMNLNHNEAPWAVYDQWQ 120
OY 217 ECKCHGSGSCYRPTGWRMLPLPAV-DVLRDFGASRVLYG--SYSSRA-----ZG 266
D 121 FCKCHGSGSCYRKTQWMLPFPVILIDLKRPDGAHVASIHRNNNNHNGRPPKN 160
OY 267 -----SKATLR-----LEPEDAHRPSPHLYTEFRSPNCTYSGLST 307
D 161 FKLALISSNHSKRENRKRYGFLKPPNEHRPPGTKLYLEDSPECKNPKGI 240
OY 308 AGTGRACNSSPALDCCCLCCGGRHTRTQVTERNCSTFWHCHVSGRMTHTVLH 367
D 241 QGTHGRLCNDSMGVDCDIMCGGRHTQDEVVEFERNCSTFWHCHVSGRMTHTH 300
OY 368 ECL 370
D 301 TCV 303

RESULT 8
OY1ZT6 PRELIMINARY: PRT; 353 AA.
AC OY1ZT6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Amphimix4.
GN WNT4.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=20164611; PubMed=10706144;
RA Schubert M., Holland L.Z., Holland N.D.;
RT "Characterization of two amphioxus wnt genes (Amphimix4 and
Amphimix5) with early expression in the developing ventral nervous
system.";
RL Dev. Dyn. 217:205-215(2000).
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
EXTRACELLULAR MATRIX (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
DR EMBL: AF061973; AACB0431.1;
DR InterPro: IPR000970; Wnt_grbthfactor.
DR Pfam: PF00110; Wnt1.1.
DR SMART: SM00097; WNT1.1.
DR PROSITE: PS00246; WNT1.1.
KW Developmental protein; Glycoprotein.
SQ SEQUENCE 353 AA: 39263 MW: 6293P92029C6C3A9 CR64;

Query Match: 41.0%; Score 834; DB 5; Length 353;
Best Local Similarity 43.7%; Pred. No. 4.1e-72;
Matches 160; Conservative 65; Mismatches 117; Indels 24; Gaps 8;

OY 11 VSATLLALALPAALANSSGRWGVVAVASTNLIDSKSLQVLEISGLLSRQGR 70
D 4 INVILVFLVATVSTGSA-TANQWLELV--ASAVSVRTED-----ACEKIDHLSR-QVQ 54

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Db 182 KGNSSGRPLMNIHNNFAGKKAALHNNQVEKCHSVSSGSELCRTCKMYMPPRRVAVLKE 241  
 QY 249 PFDGASVLYGNRGSNFRASRAELLRLPEDEPAHKPPSFHDLYFEKSPNFCITYSGLTA 308  
 Db 242 HFDATFVRLKLPVGSRTA-----LLPRDQVFPATRELVLAPLSDFLDEPNJIP 294  
 QY 309 GTAGACNSSSP-ALDGCCELLCGRGHRTICQVTEKNCQTFHMCQVSCNCTHTPYLH 357  
 Db 295 GTAGRCNCTSLAPDGTCLLCGCGPFRARAEVYGRSCSKFSCSVRCQCKNTVLIH 354  
 QY 368 EC 369  
 Db 355 TC 356

## RESULT 13

080M39 PRELIMINARY: PRT: 350 AA.  
 AC 080M39.  
 DT 01-MAR-2002 (TEMBLrel: 20, Created)  
 DT 01-MAR-2002 (TEMBLrel: 20, Last sequence update)  
 DT 01-JUN-2002 (TEMBLrel: 21, Last annotation update)  
 DE WNT2 protein.  
 GN WNT2.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthopterygii; Acanthopterygii; Perciformes; Tetraodontiformes;  
 OC Tetraodontidae; Takifugu.  
 OC NCBI\_TaxID=31033;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Aveile K., Beckstrom-Sternberg S.M., Benjamin B., Blakesley R.W.,  
 RA Bouffard G.G., Eren K., Brinkley C., Brooks S., Dietrich N.L.,  
 RA Granite S., Guan X., Gupta J., Ho S.-L., Idol J.R., Kallins E.,  
 RA Lee-Lin S.-Q., Legaspi R., Lim M., Maduro Q.L., Maduro V.B.,  
 RA Masello G., Mastrian S.D., McCloskey J.C., McDevell J., Pearson R.,  
 RA Prasad A., Shevchenko Y., Snyder B., Stantitop S., Thomas J.W.,  
 RA Thomas P.J., Touchman J.W., Tsurganov G., Vogt J.L., Walker M.A.,  
 RA Wetherly K.D., Zhang L.-H., Green E.D.;  
 RA "NISC Comparative Sequencing Initiative";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AC091272; AAL40358.1;  
 DR InterPro: IPR000345; Cytochrome\_bind.  
 DR InterPro: IPR006970; Wnt\_gtf\_factor.  
 DR Pfam: PF00110; Wnt\_1.  
 DR PRINTS: PR01349; WNTPROTEIN.  
 DR SMART: SM00097; WNT1.1.  
 DR PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN.1.  
 DR PROSITE: PS00246; WNT1; UNKNOWN.1.  
 SQ SEQUENCE 350 AA: 38953 MW: 75AB34B82B03D3BD CRC64;

Query Match 38.3% Score 779; Dh 13; Length 350;  
 Best Local Similarity 41.0%; Pred. No. 8, 36-67;  
 Matches 152; Conservative 62; Mismatches 121; Indels 36; Gaps 7;

QY 7 LFGWVSATLLALALPALAANSSGRWMDIVVASTNILLTDSASQVLEPSLISLR 56  
 Db 4 VPSGICEFVSVALCMLTAEDVAS---WMYMGTLISGQ-----VMCDNIPGLVN 47  
 QY 67 KQRLIRONGPGLHSVSGGLQSAVECKMOPFRNPNKCTAPGPH-LEQKIVNRGRTFA 125  
 Db 48 KQRLCROHPKVMQATIGSGIKWISIECHQFRNHNKNCITARRHNLFGELLRSSREVA 107  
 QY 126 FIFATTSAGVTHSVANSGSEGISCTGCTVRRRQGP---DMHMGCSNIDFGRLPR 182  
 Db 108 FTYALSSAGVYVALARACSGDLDSCDPAKKGSSROAKGSFSGSDSHVHAMFSG 167  
 QY 183 EFVDSGE-KGRDLRFLMLNHNNEAGRTVSEMRQECQCHQSGSCTVTCMMRLDTLFA 241  
 Db 168 AFVDAKERKERDAPALMLNHNRRAGRAVREMTLECKCHGVSSGSCSFCGWSAMADFRR 227  
 QY 242 VQDVLRKRFQDASVLYGNRGSNFRASRAELLRLPEDEPAH---KPPSFHDLYFEKSPNF 298

Db 228 TGRHLEPKRYNGAVYAVWQVCTGTT-----AHMHRKLFQSKMLVYLEDSYD 275  
 QY 299 CTYSGRILGTAGTRACNSSPALDGCCELLCGRKHRTPLVTEKNCITFMQCHVSCR 358  
 Db 276 CVRQDGSGLGTGQJLCNRTSPGIDGCEVWGCRGDTSPVQTIKCEKTFHMCQAVLCR 345  
 QY 359 NCTHTPYLHPC 369  
 Db 336 DCHQVAVHTC 346

## RESULT 14

098SN7 PRELIMINARY: PRT: 385 AA.  
 AC 098SN7.  
 DT 01-JUN-2001 (TEMBLrel: 17, Created)  
 DT 01-JUN-2001 (TEMBLrel: 17, Last sequence update)  
 DT 01-JUN-2002 (TEMBLrel: 21, Last annotation update)  
 DE Wq/Int-1 related gene product Wnt-2b.  
 GN Wnt-2b.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDJIANE-21759450; FdbMed2-1209326;  
 RA Kawakami Y., Capdeville C., Fischer S., Itoh T., Ezura Y.,  
 RA Holmberg J.O.;  
 RA "Wnt signaling controls PIF-dependent limb initiation and AER induction  
 in the chick embryo";  
 RL Cell 103:471-483(2001).  
 CC - FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).  
 CC - SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE  
 CC - EXTRACELLULAR MATRIX (BY SIMILARITY).  
 CC - SIMILARITY: BELONGS TO THE WNT FAMILY.  
 DR EMBL: AF445628; AAK3108.1;  
 DR F0149628; AAK3108.1;  
 DR InterPro: IPR000970; Wnt\_gtf\_factor.  
 DR Pfam: PF00110; Wnt\_1.  
 DR PRINTS: PR01349; WNTPROTEIN.  
 DR SMART: SM00097; WNT1.1.  
 DR PROSITE: PS00246; WNT1; UNKNOWN.1.  
 KM Nucleoprotein protein; Glycoprotein.  
 SQ SEQUENCE 385 AA: 42952 MW: FE3264C0EAB3F6E5 Dc744;

Query Match 38.0% Score 774.5; Dh 13; Length 385;  
 Best Local Similarity 41.3%; Pred. No. 2, 56-56;  
 Matches 149; Conservative 64; Mismatches 155; Indels 33; Gaps 8;

QY 15 LIALALPALAALANSSGRWMDIVVASTNILLTDSASQVLEPSLISLR 74  
 Db 40 VILLALTPA-----LSSMWYALCAR-----VIGNLPLVYKQVQULOR 82  
 QY 75 NPGILHSVSGGLQSAVECKMOPFRNPNKCTAPGPH-LEQKIVNRGRTFAFIATISA 133  
 Db 83 YELINQSVGEATFMLEQVGFQFRHNMNCSTLDRLHVFQVWVLRSPRAAVATISA 142  
 QY 134 GVTASVARSSEGISIECTGVRRRRQGP---DMHMGCSNIDFGRLPR 190  
 Db 143 GYVAVALTACSGGLALACGCPLEKRGAKDERGEFWMGSCSNINYIIPRAVFIAREK 202  
 QY 191 G-KRLRFLMLNHNNEAGRTVSEMRQECQCHQSGSCTVTCMMRLDTLFA 249  
 Db 203 KYKDFALMLNHNRRAGRAVREMTLECKCHGVSSGSCSFCGWSAMADFRR 227  
 QY 250 PFGASVLYGNRGSNFRASRAELLRLPEDEPAHKPPSFHDLYFEKSPNFCTYSGLTAG 309  
 Db 263 YGALVLYNMQDGT-----FVANKRFRKPTKTNLYFENSDYVVMKSA3SLG 313  
 QY 311 TAGRCNSSSPALDGCCELLCGRKHRTPLVTEKNCITFMQCHVSCR 369

